Fig.1

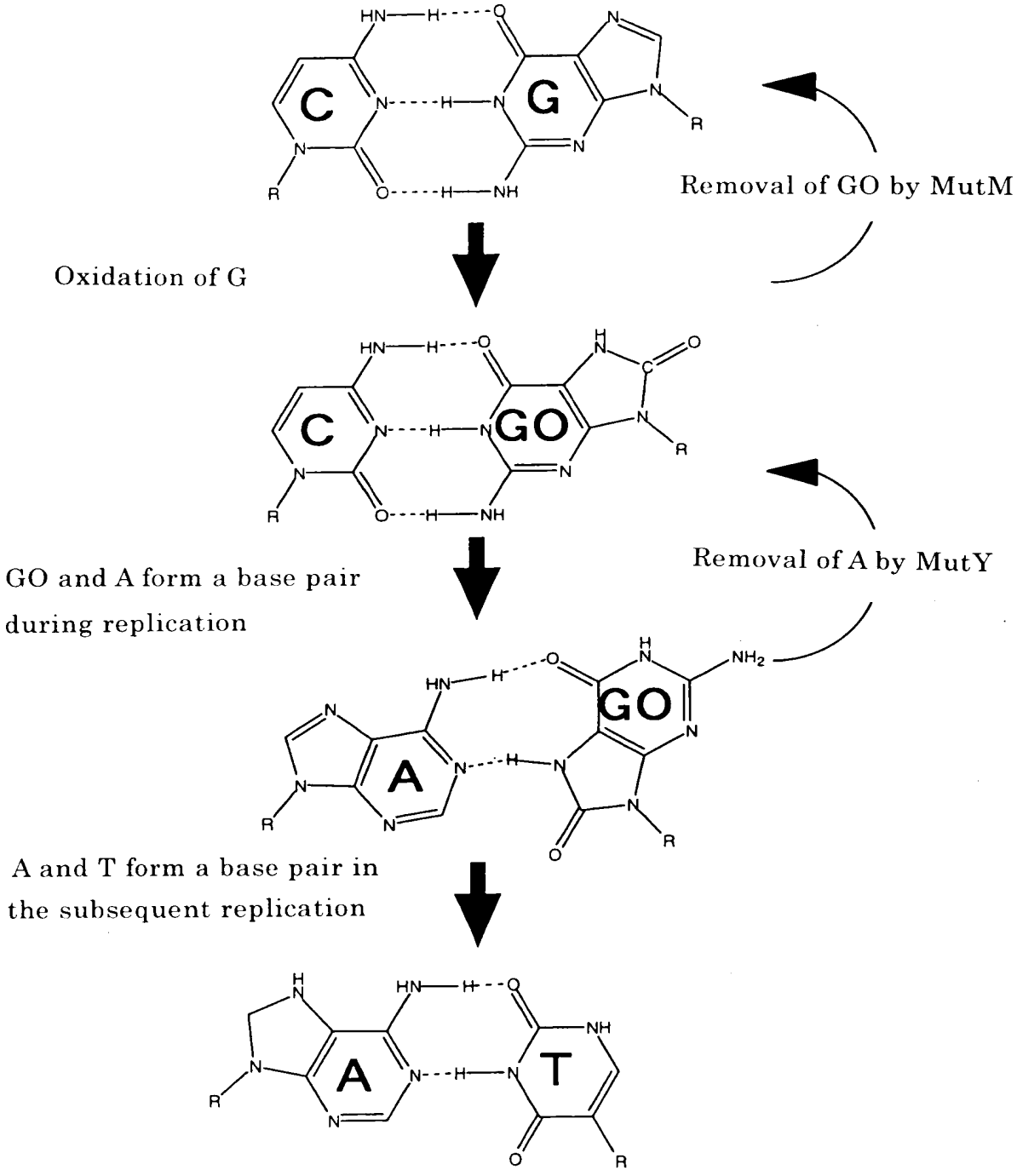

C
G
Removal of GO by MutM
Oxidation of G
C
GO
GO and A form a base pair during replication
Removal of A by MutY
A
GO
A and T form a base pair in the subsequent replication
A
T

Fig.2

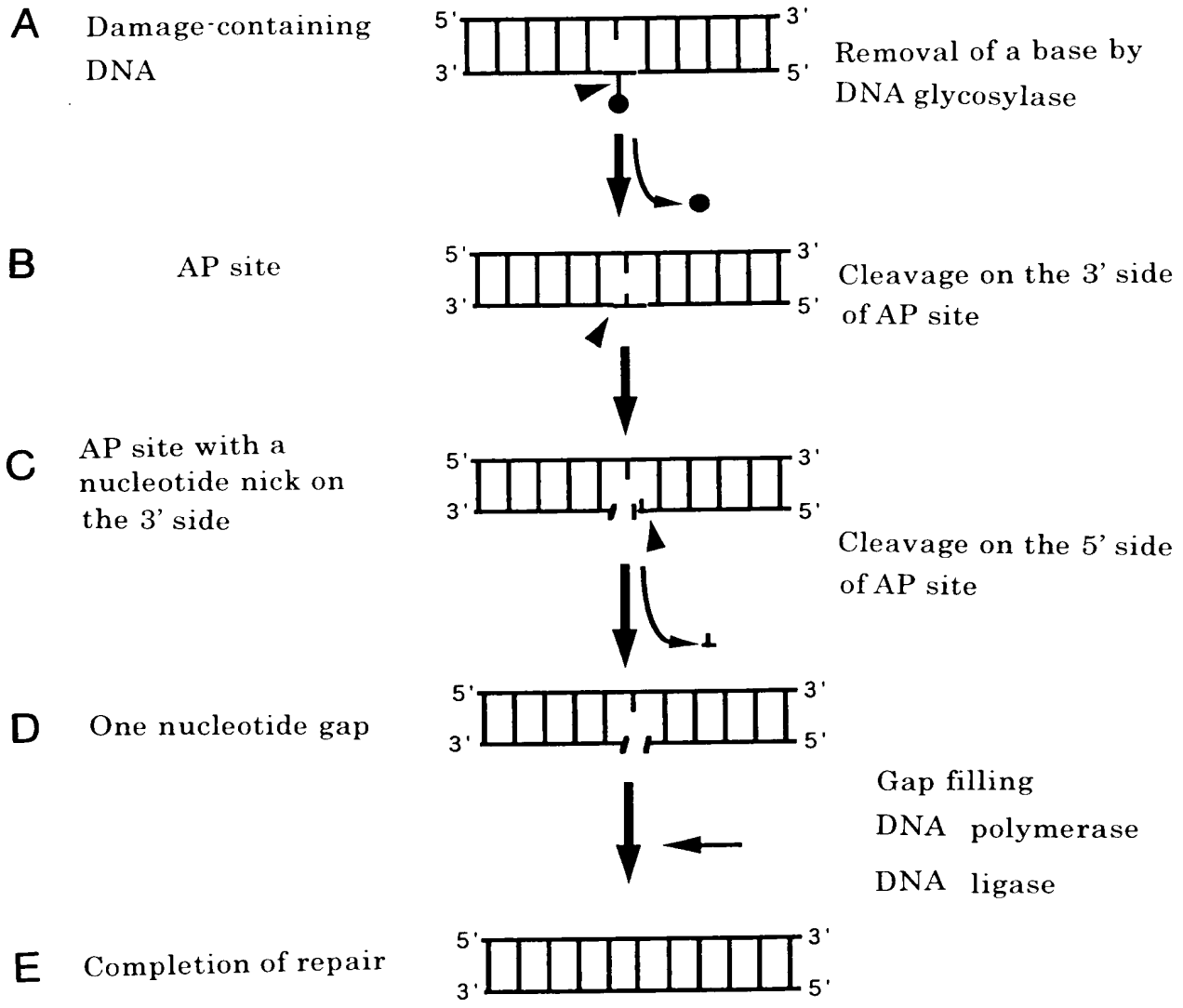

A
Damage-containing DNA
5'
3'
3'
5'
Removal of a base by DNA glycosylase
B
AP site
Cleavage on the 3' side of AP site
C
AP site with a nucleotide nick on the 3' side
Cleavage on the 5' side of AP site
D
One nucleotide gap
Gap filling
DNA polymerase
DNA ligase
E
Completion of repair

Fig.3

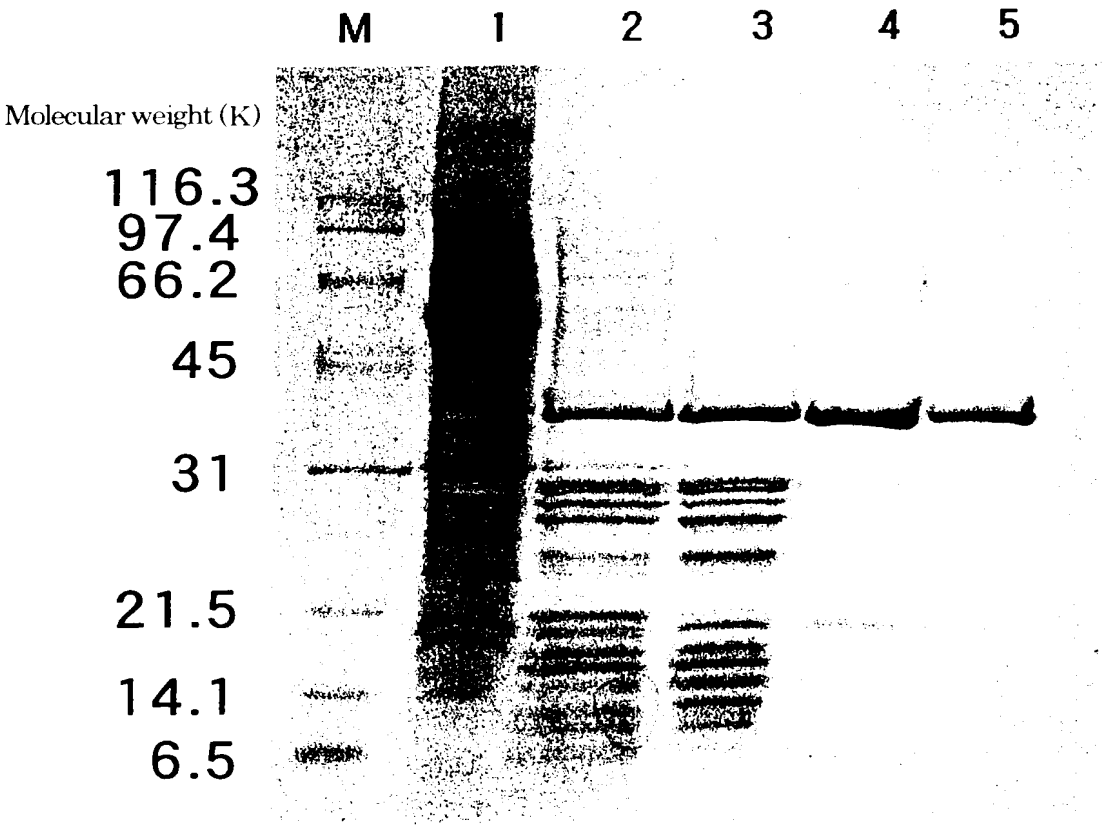


Fig.4

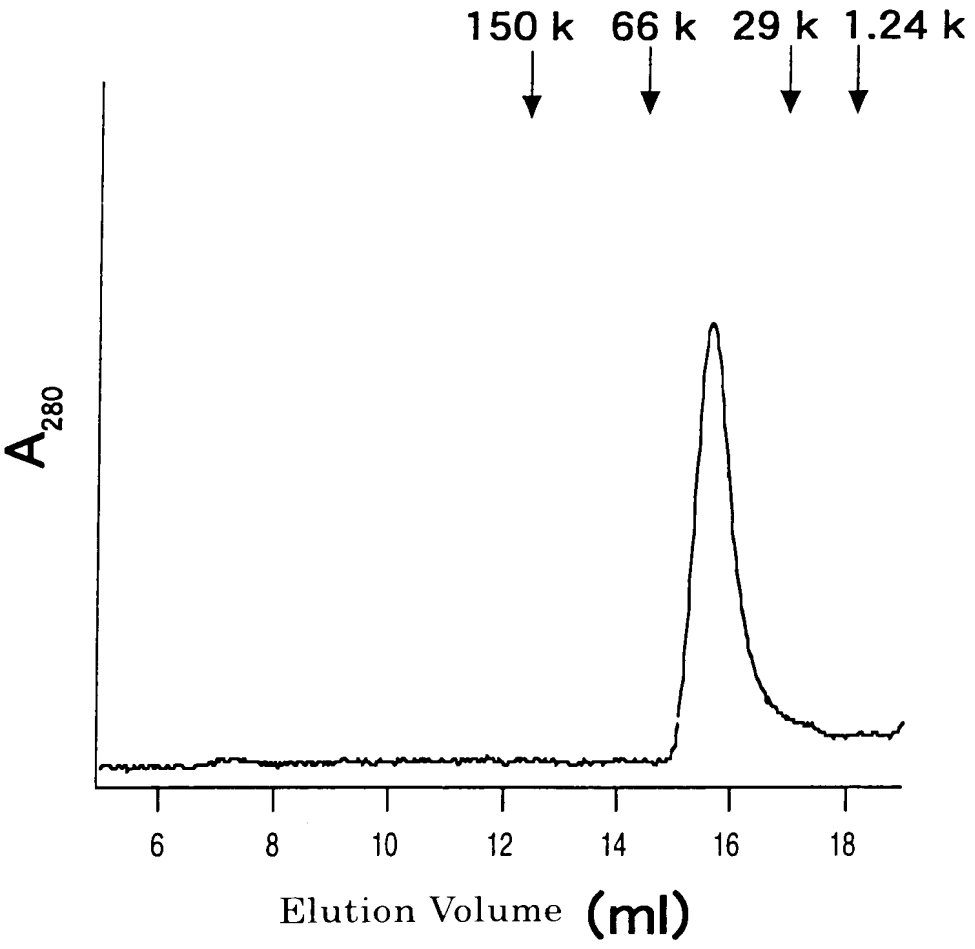
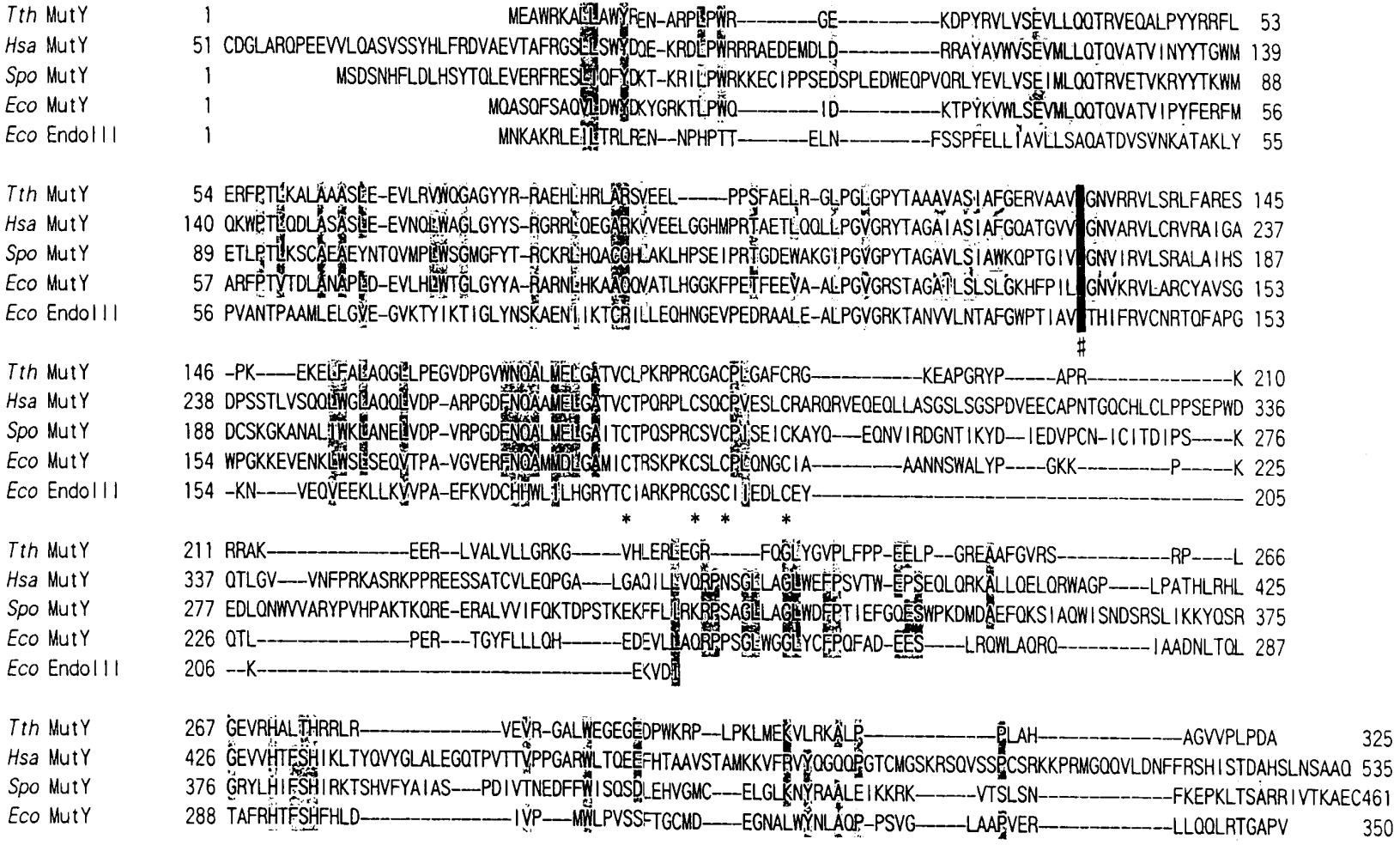


Fig.5

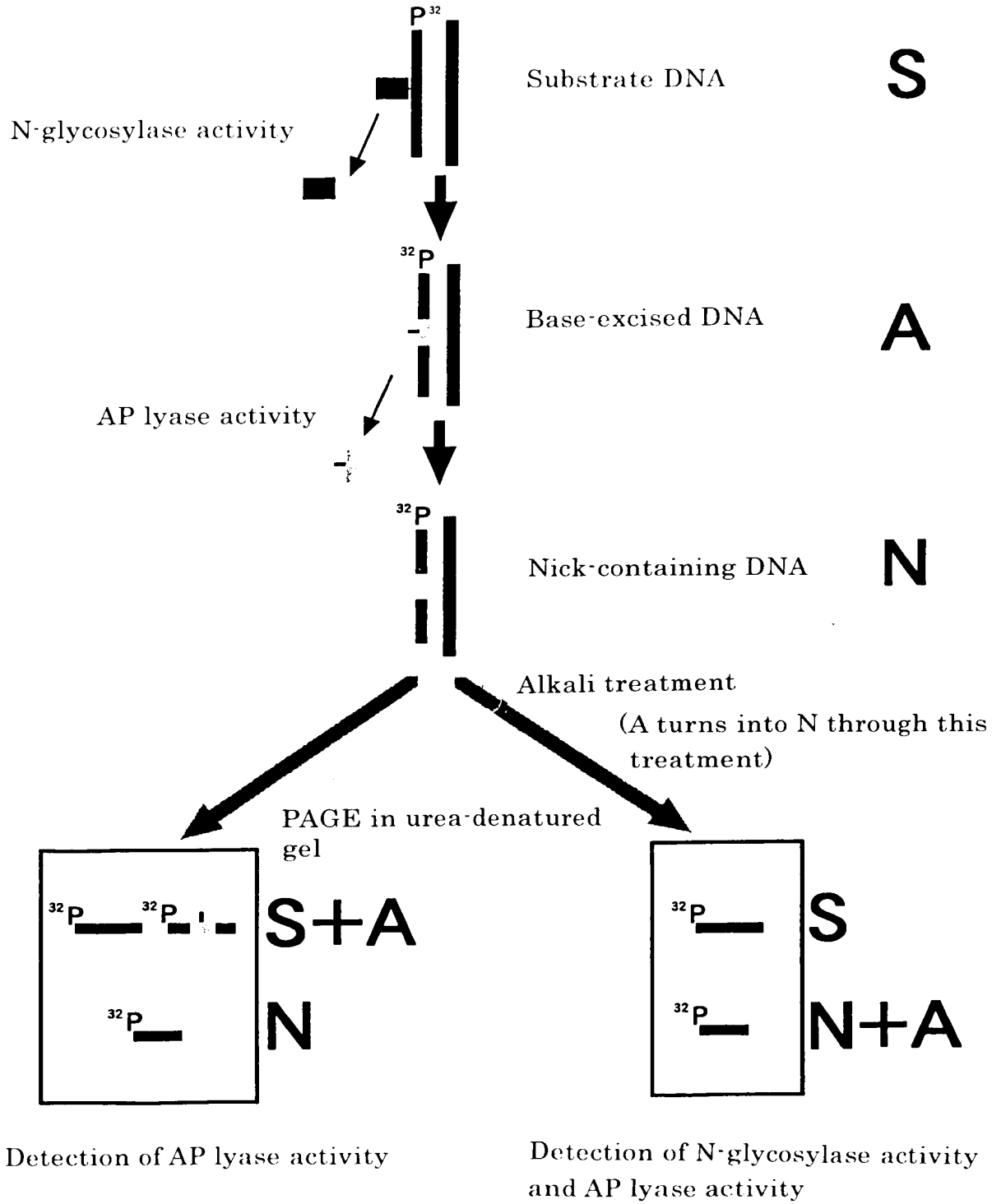


Tth (*Thermus thermophilus* HB8), *Hsa* (Homo *sapiens*), *Spo* (*Schizosaccharomyces pombe*), *Eco* (*Escherichia coli*)

Residue essential for N-glycosylase activity * Residues constituting an iron-sulfur cluster

(D)

Fig.6


P32
Substrate DNA
S
N-glycosylase activity
32P
Base-excised DNA
A
AP lyase activity
32P
Nick-containing DNA
N
Alkali treatment
(A turns into N through this treatment)
PAGE in urea-denatured gel
32P 32P
S+A
32P
N
32P
S
32P
N+A
Detection of AP lyase activity
Detection of N-glycosylase activity and AP lyase activity

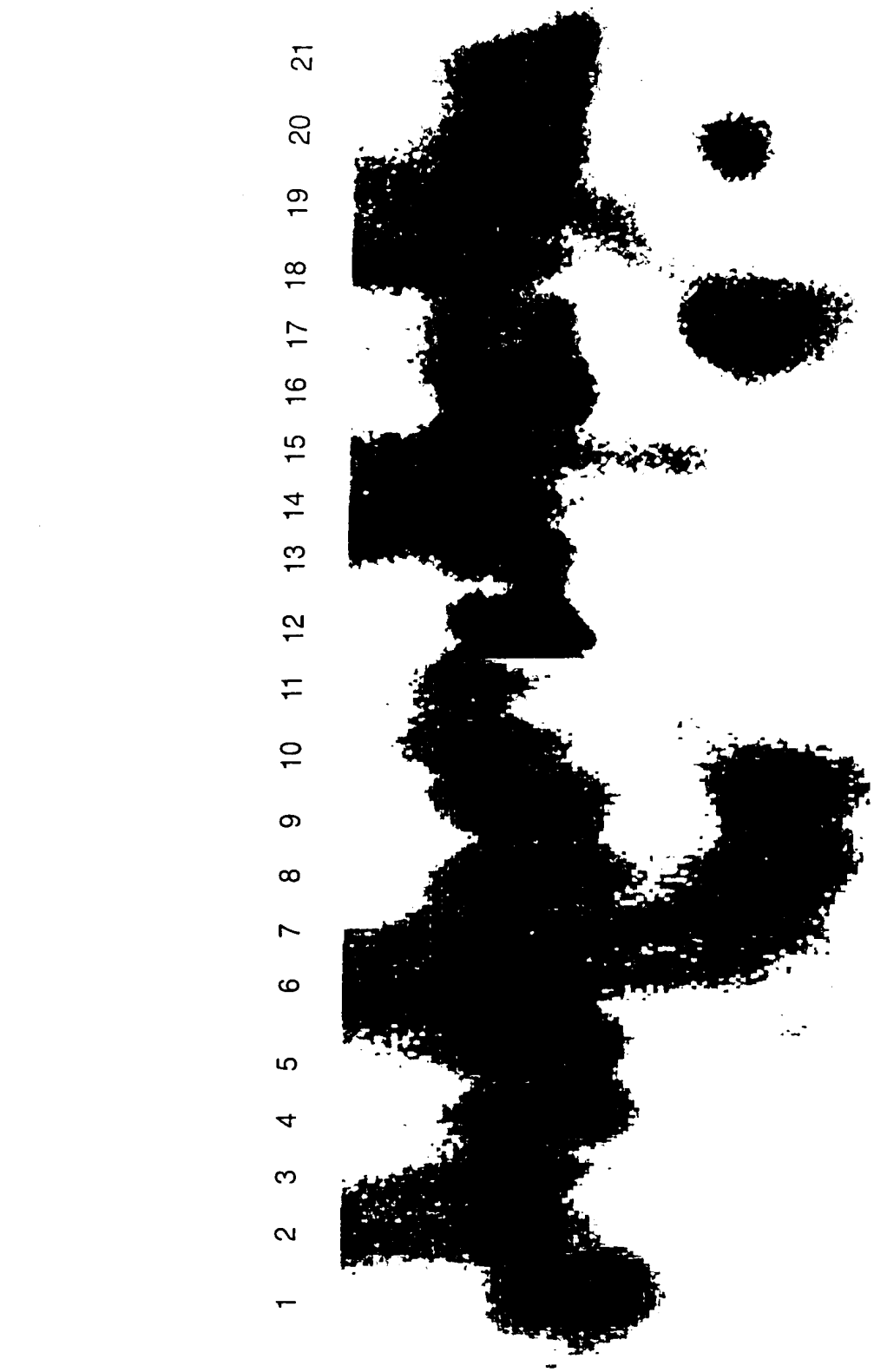


Fig.7

Fig.8

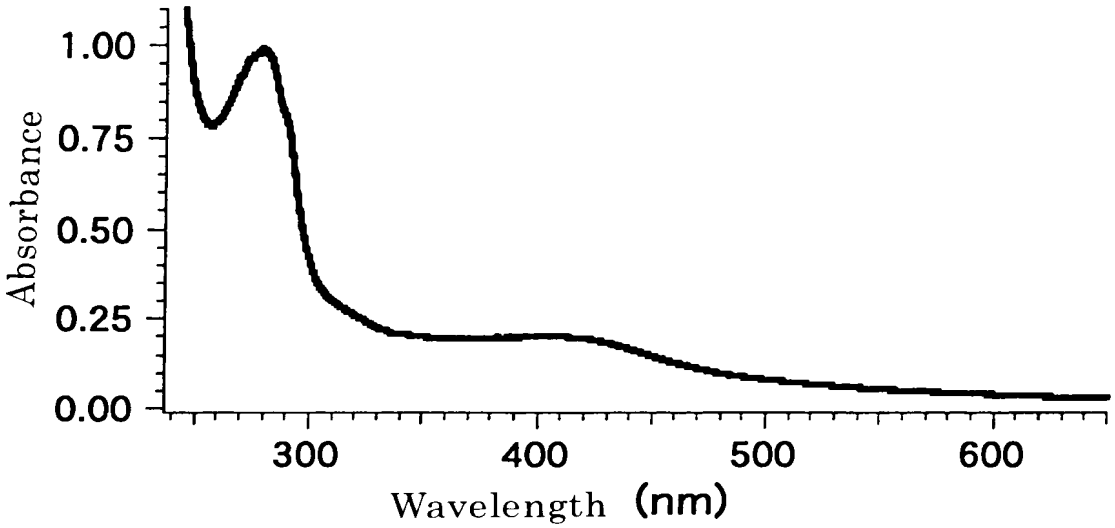

1.00
0.75
0.50
0.25
0.00
Absorbance
300
400
500
600
Wavelength (nm)

Fig.9

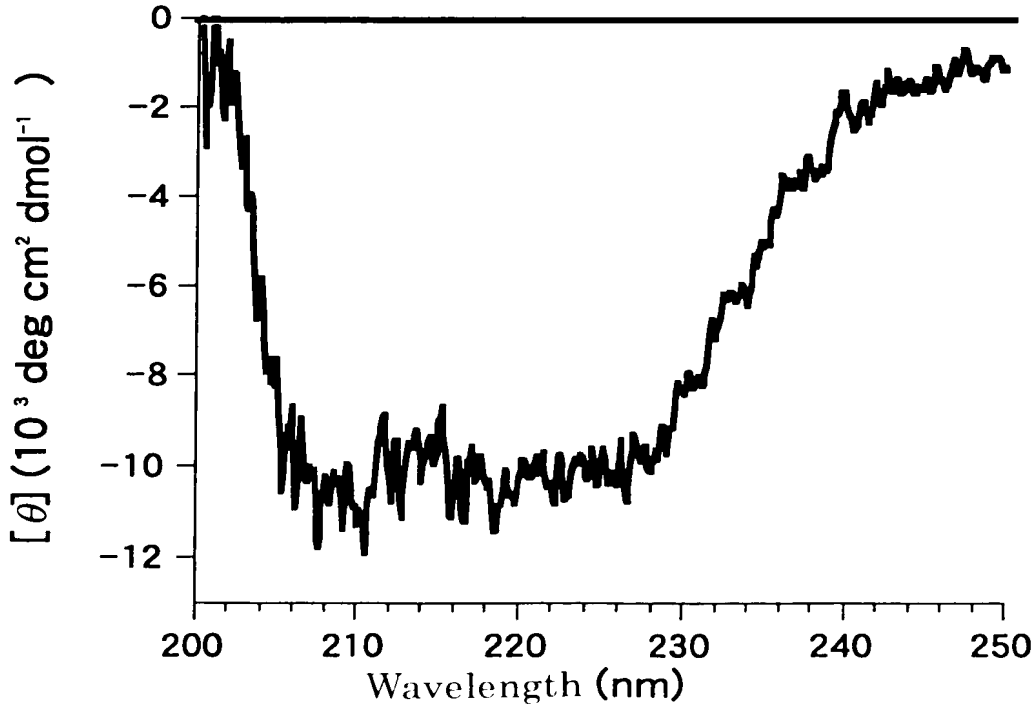

0
-2
-4
-6
-8
-10
-12
[θ] (10³ deg cm² dmol⁻¹)
200
210
220
230
240
250
Wavelength (nm)

Fig.10

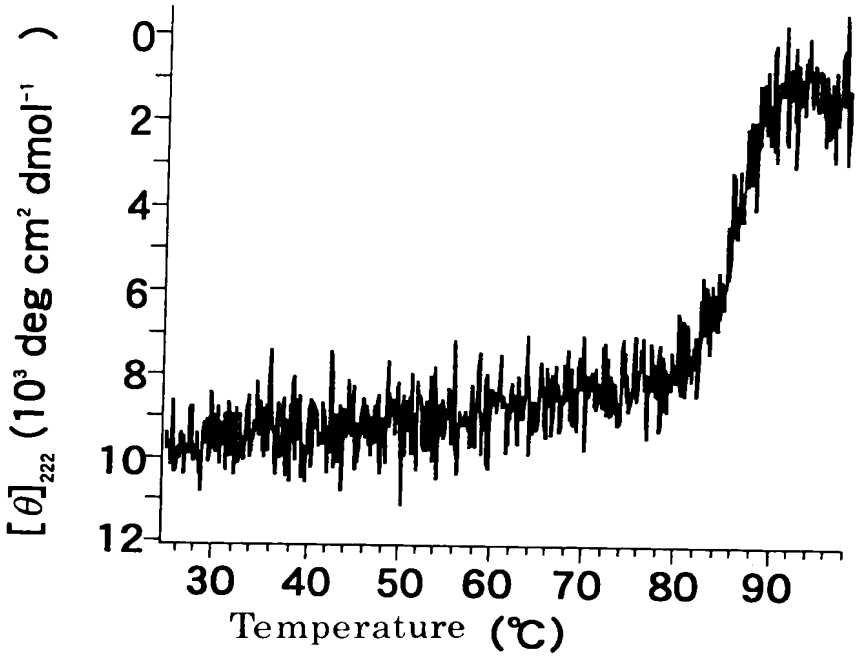

$[\theta]_{222}$ (10^3 deg cm^2 dmol^{-1})
0
2
4
6
8
10
12
30
40
50
60
70
80
90
Temperature (℃)

Fig.11

5' -[^{32}P]AGATCTTGACGGGGAAAYCCGAATTCGGCGAACGTGGCGAG-3'
3' -AATCTAGAACTGCCCCTTTXGGCTTAAGCCGCTTGCACCGCTCTT-5'

X : GO, G, C, T Y : A, G

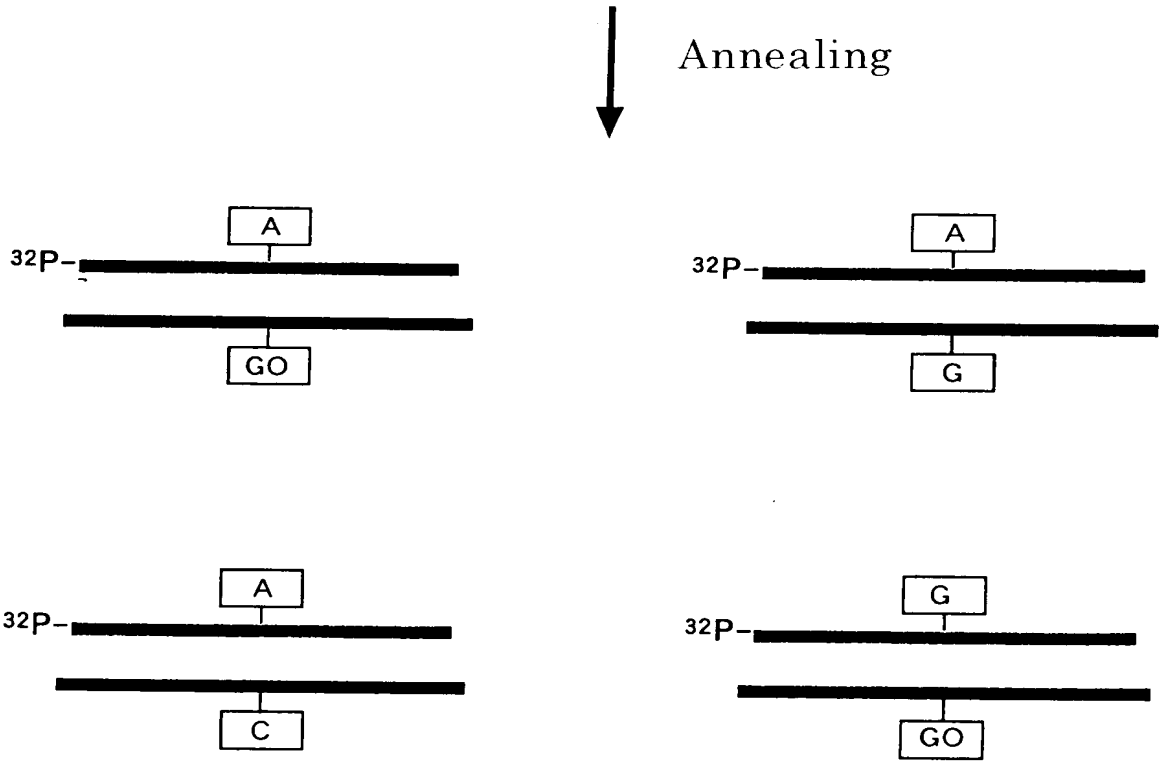


Fig.12

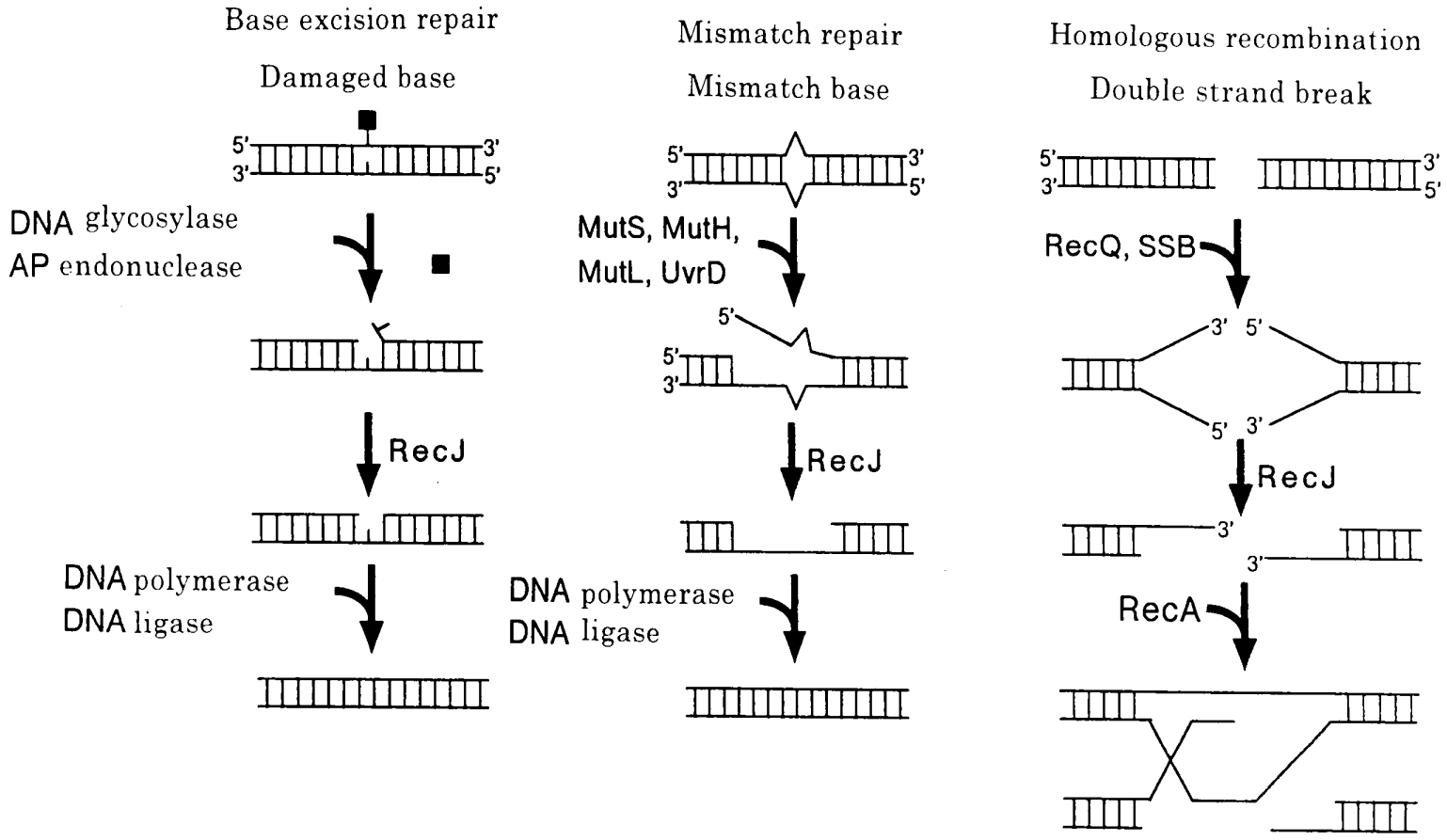

Base excision repair
Damaged base
5'
3'
3'
5'
DNA glycosylase
AP endonuclease
RecJ
DNA polymerase
DNA ligase
Mismatch repair
Mismatch base
MutS, MutH,
MutL, UvrD
RecJ
DNA polymerase
DNA ligase
Homologous recombination
Double strand break
RecQ, SSB
RecJ
RecA

Fig.13

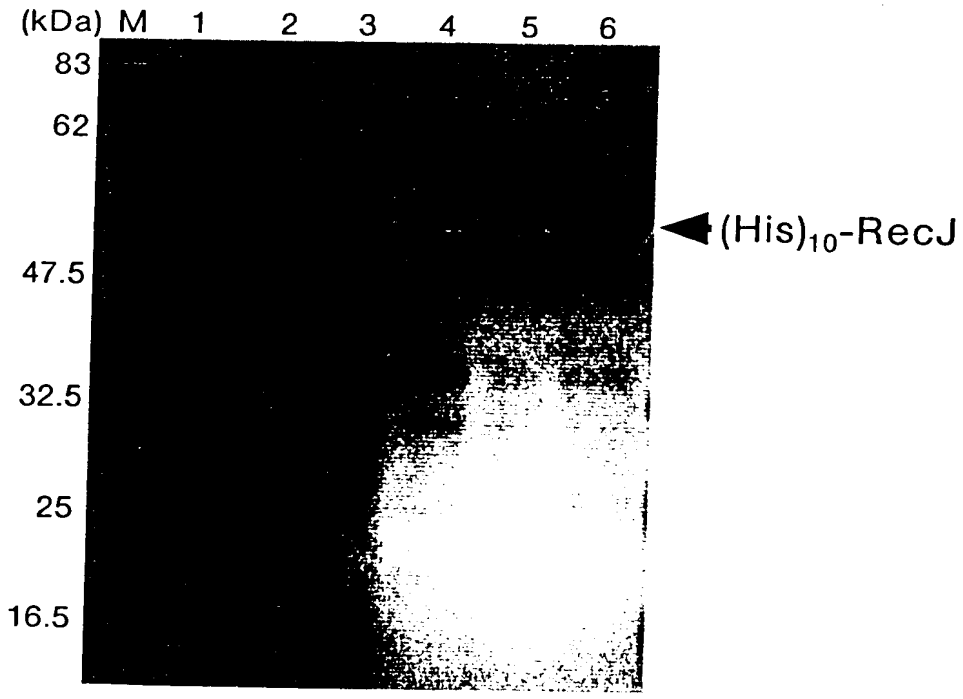
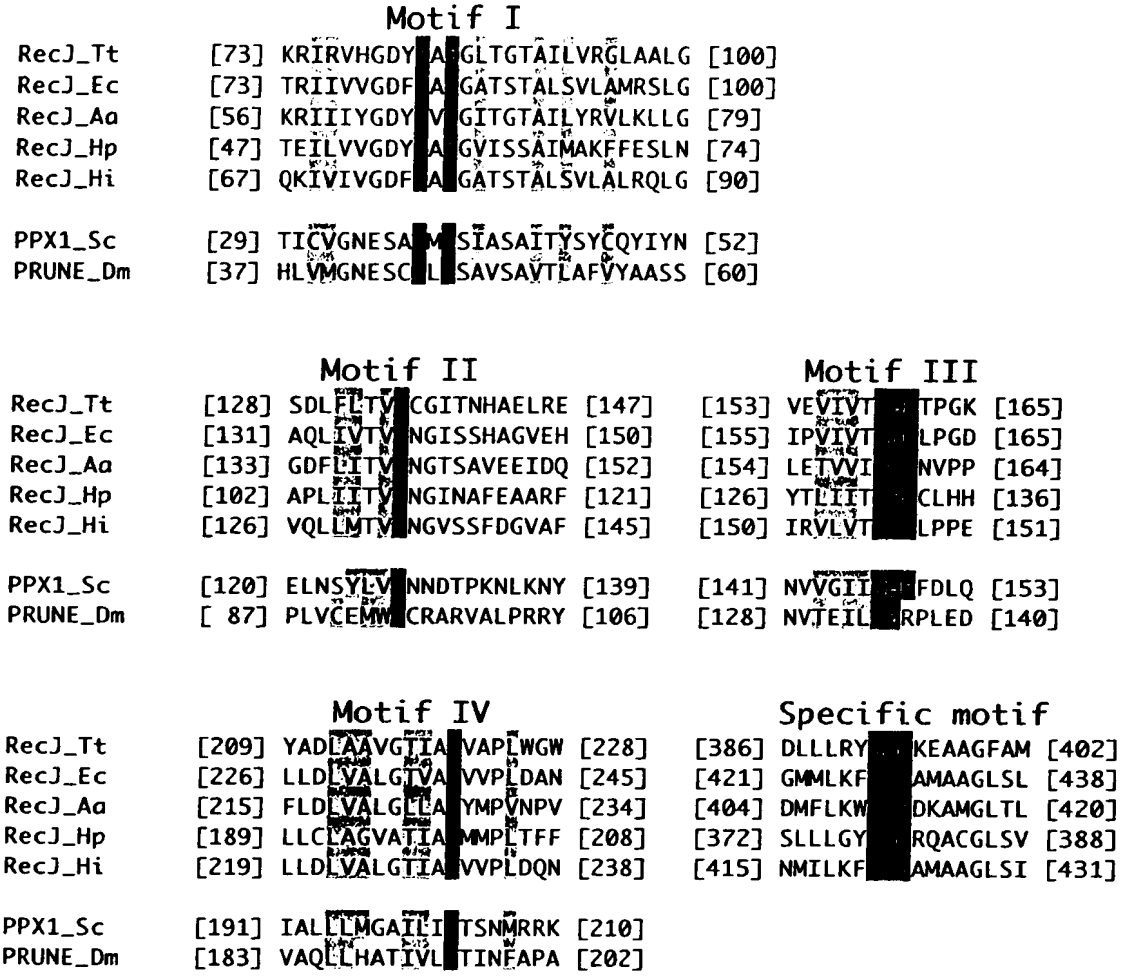


Fig.14



Tt : *Thermus thermophilus* HB8, Ec : *Escherichia coli*, Aa : *Aquifex aeolicus*,
Hp : *Helicobacter pyroli*, Hi : *Haemophilus influenzae* Rd,
Sc : *Saccharomyces cerevisiae*, Dm : *Drosophila melanogaster*

Fig.15

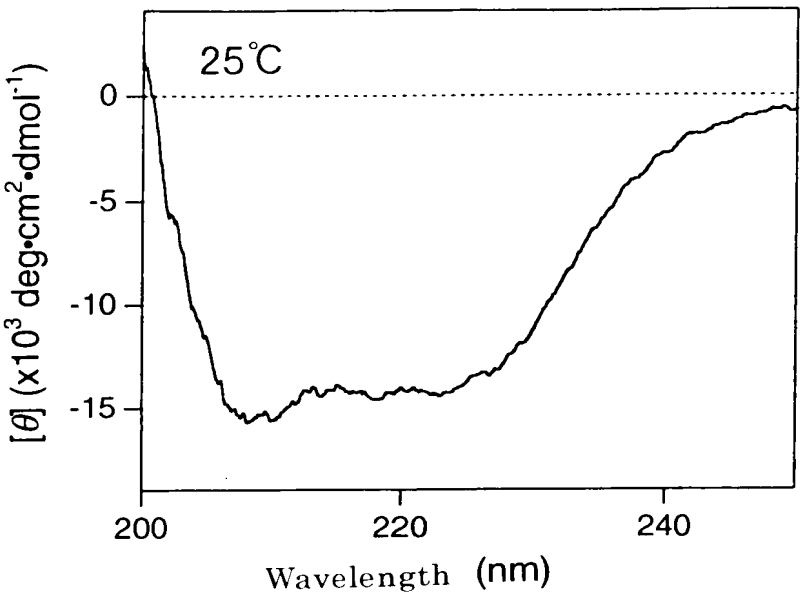

25℃
0
-5
-10
-15
[θ] (x10³ deg•cm²•dmol⁻¹)
200
220
240
Wavelength (nm)

Fig.16

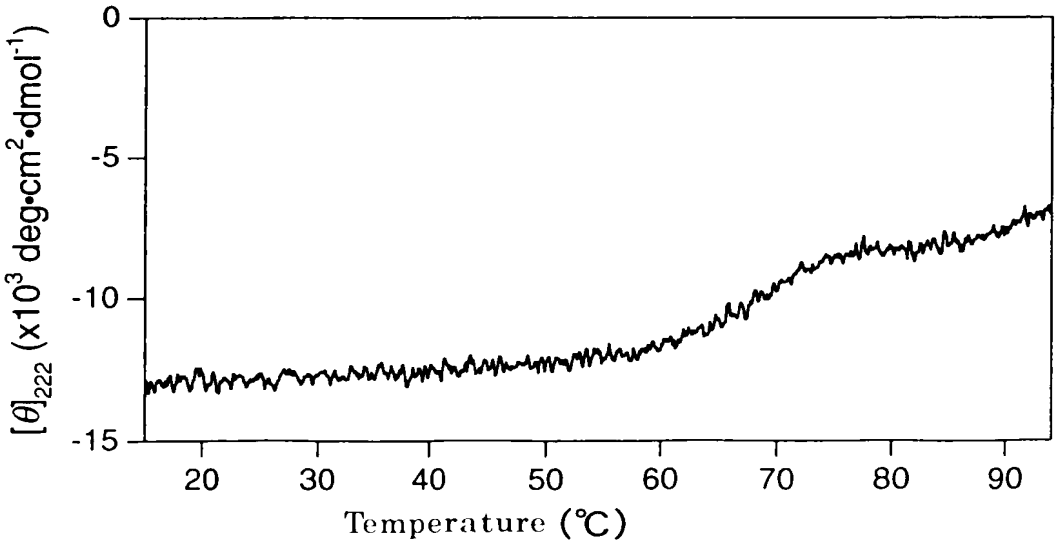

0
-5
-10
-15
[θ]222 (x10³ deg•cm²•dmol⁻¹)
20
30
40
50
60
70
80
90
Temperature (℃)

Fig.17

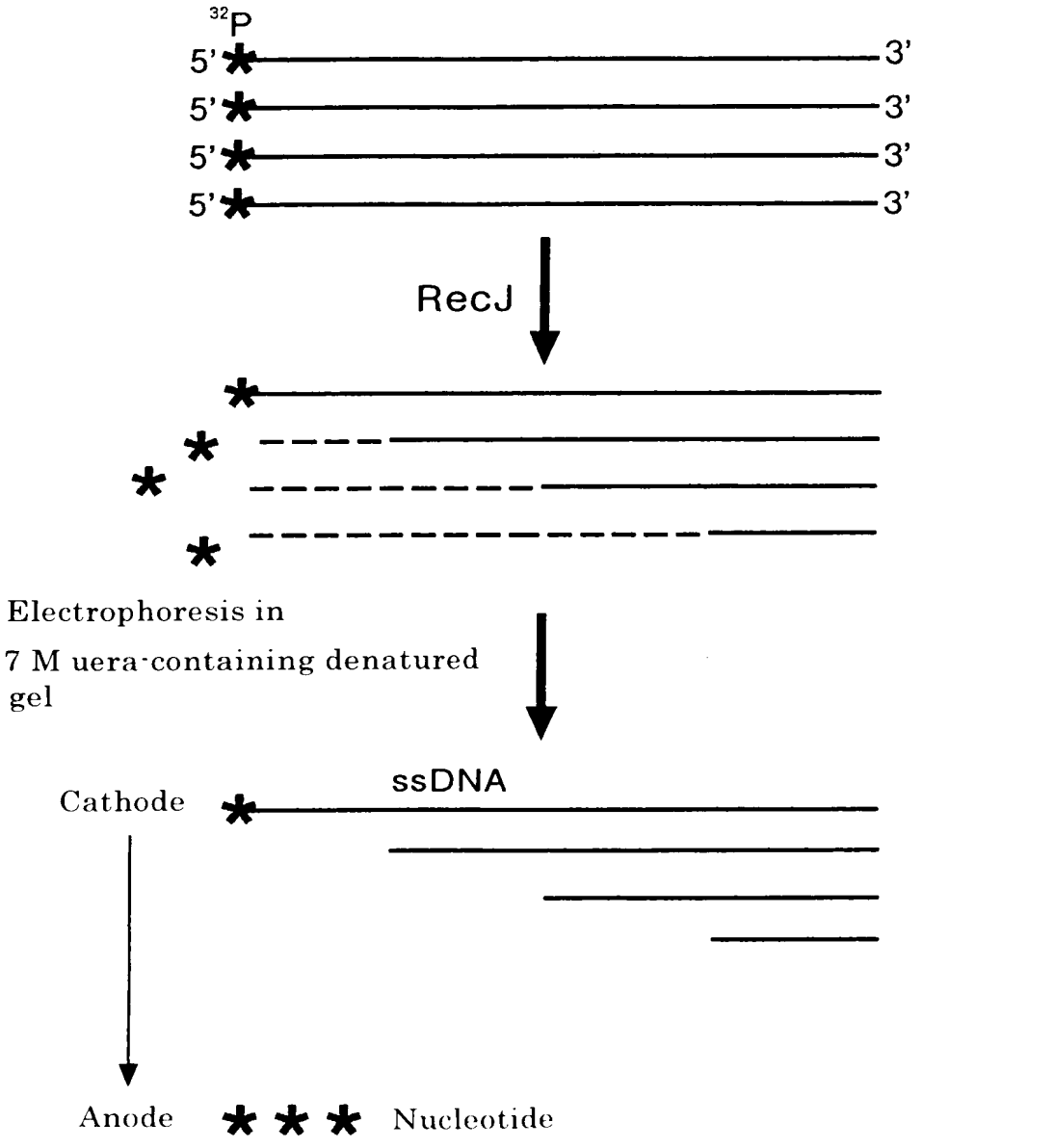

Substrate DNA : 49-mer ssDNA
5'-ACTACTTGGTACACTGACGCGAGCACGCAGGAGCTCATTCCAGTGCGCA-3'
32P
5'
3'
RecJ
Electrophoresis in
7 M uera-containing denatured
gel
ssDNA
Cathode
Anode
Nucleotide

Fig.18

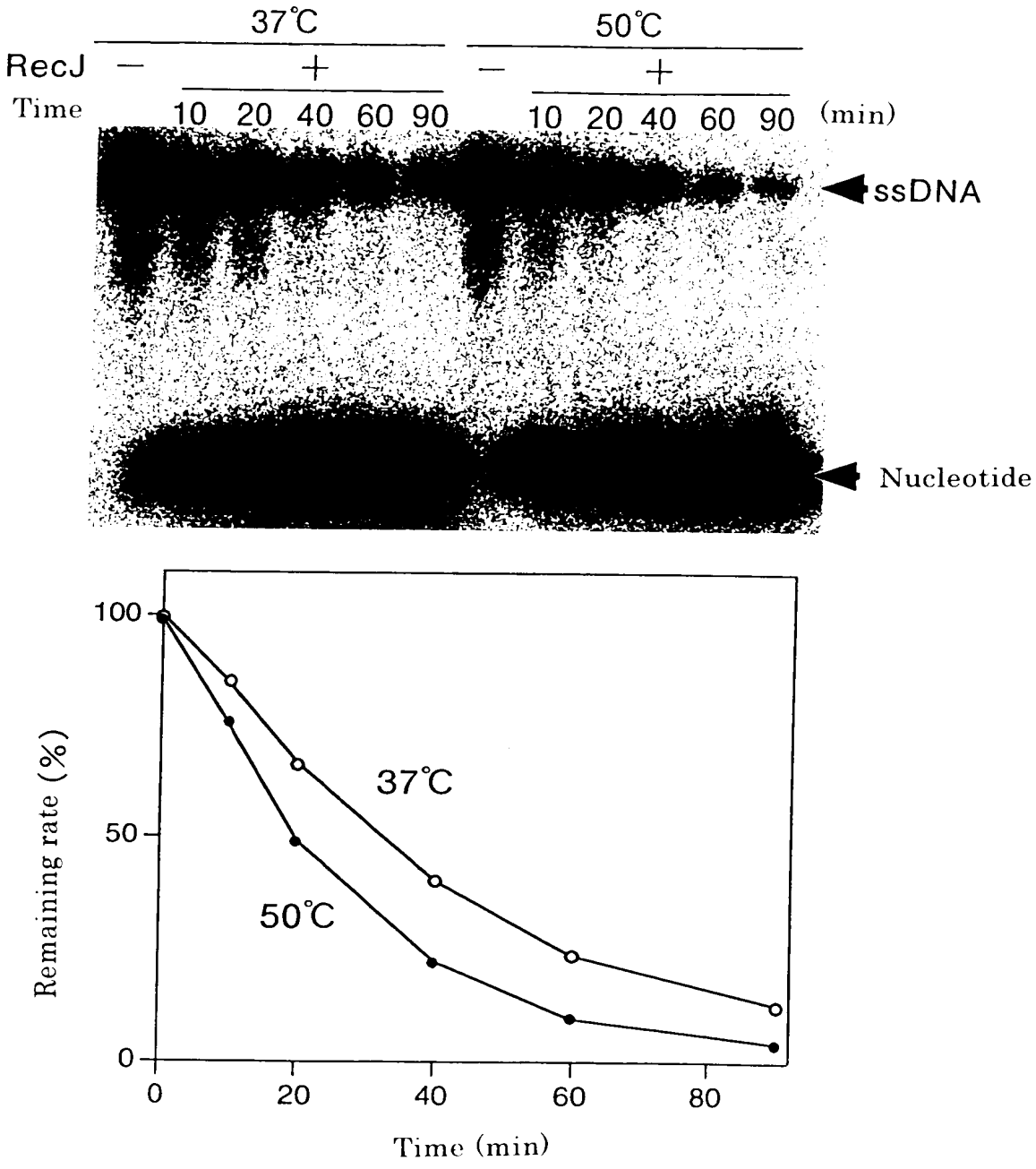

37℃
50℃
RecJ
−
+
−
+
Time
10 20 40 60 90
10 20 40 60 90
(min)
ssDNA
Nucleotide
100
50
0
Remaining rate (%)
37℃
50℃
0
20
40
60
80
Time (min)

Fig.19

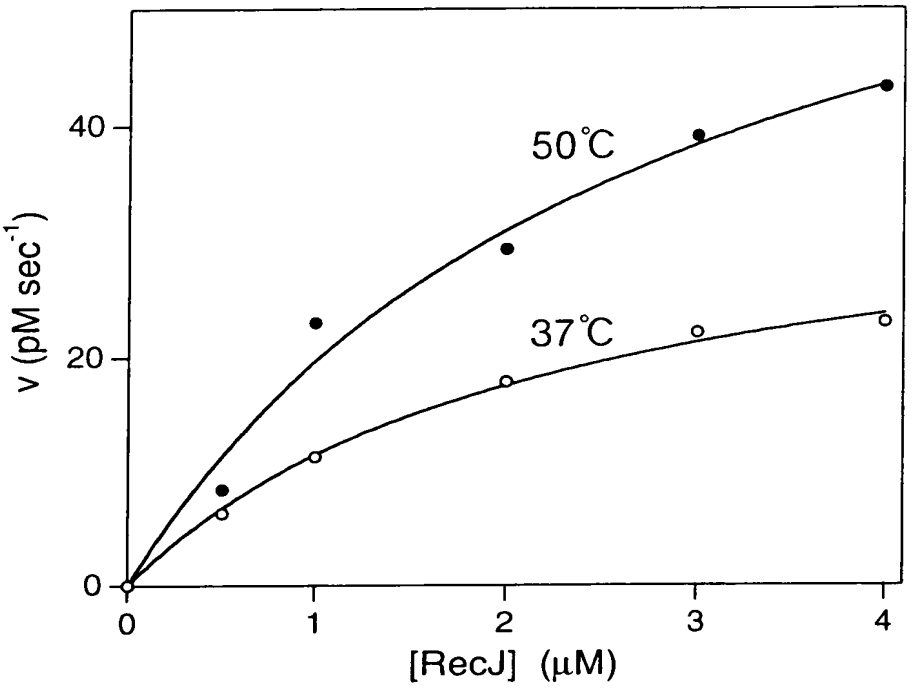


Fig.20

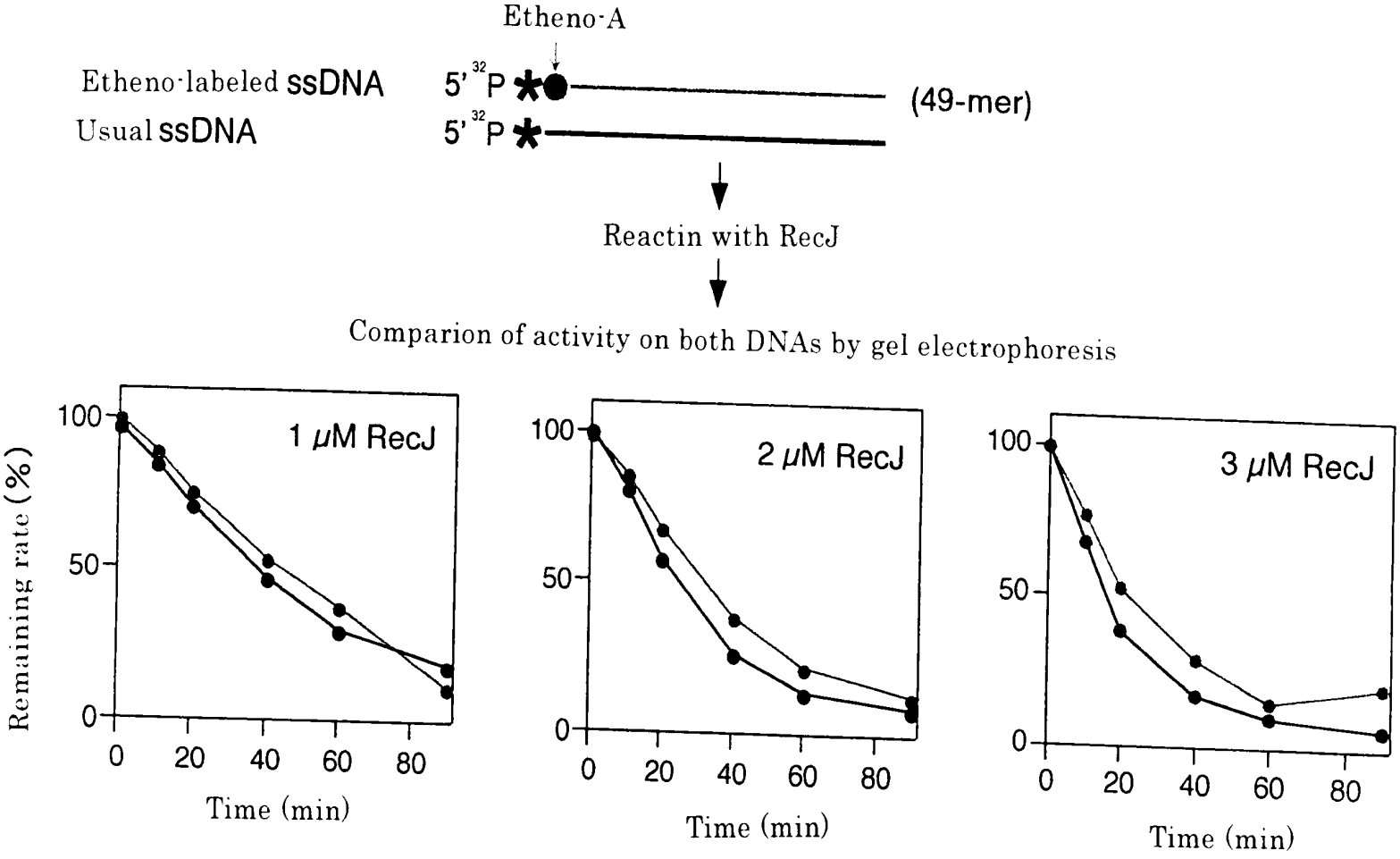

Etheno-A
Etheno-labeled ssDNA
5' 32P
(49-mer)
Usual ssDNA
5' 32P
Reactin with RecJ
Comparion of activity on both DNAs by gel electrophoresis
Remaining rate (%)
100
50
0
1 μM RecJ
2 μM RecJ
3 μM RecJ
0
20
40
60
80
Time (min)

Fig.21

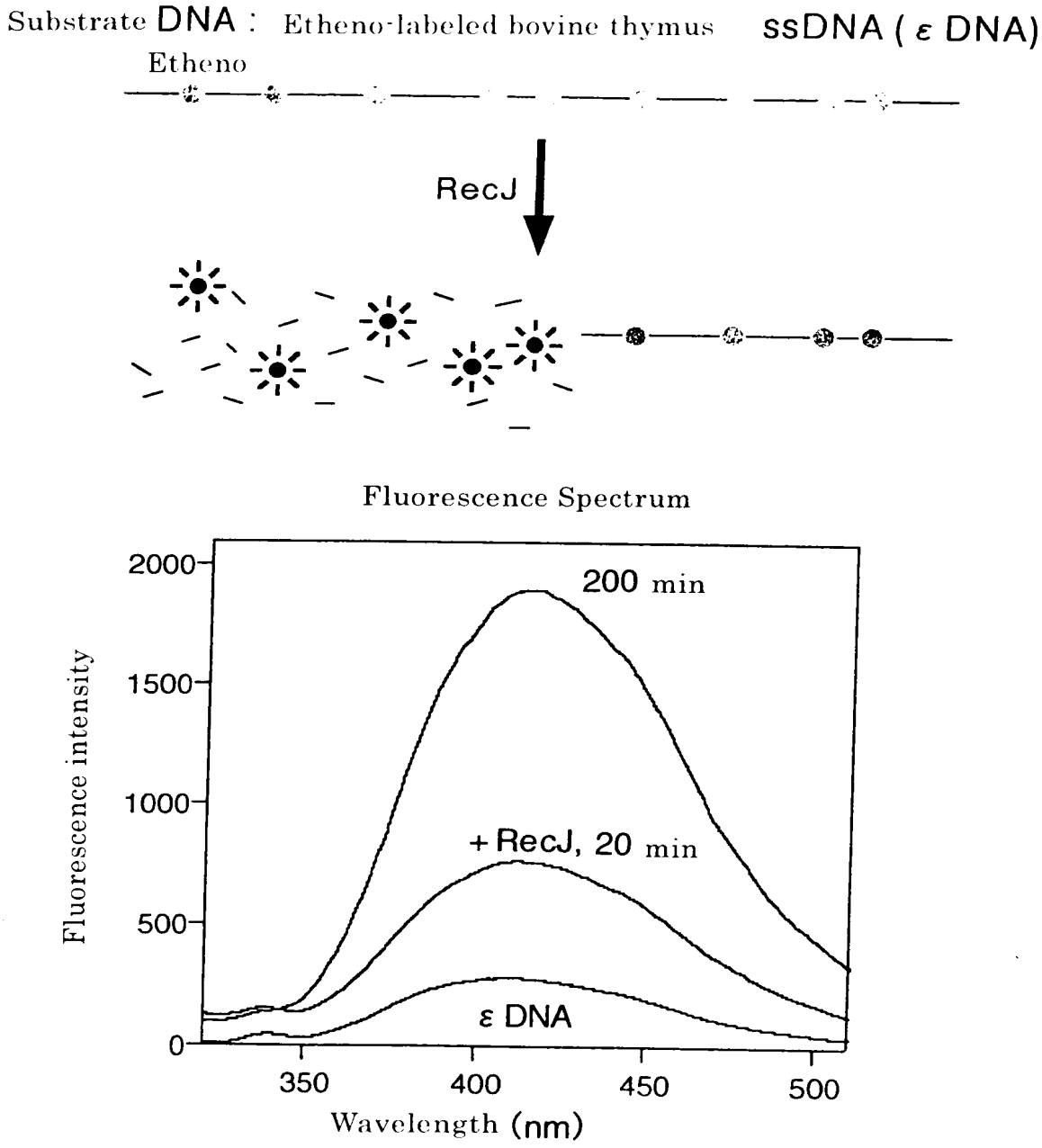
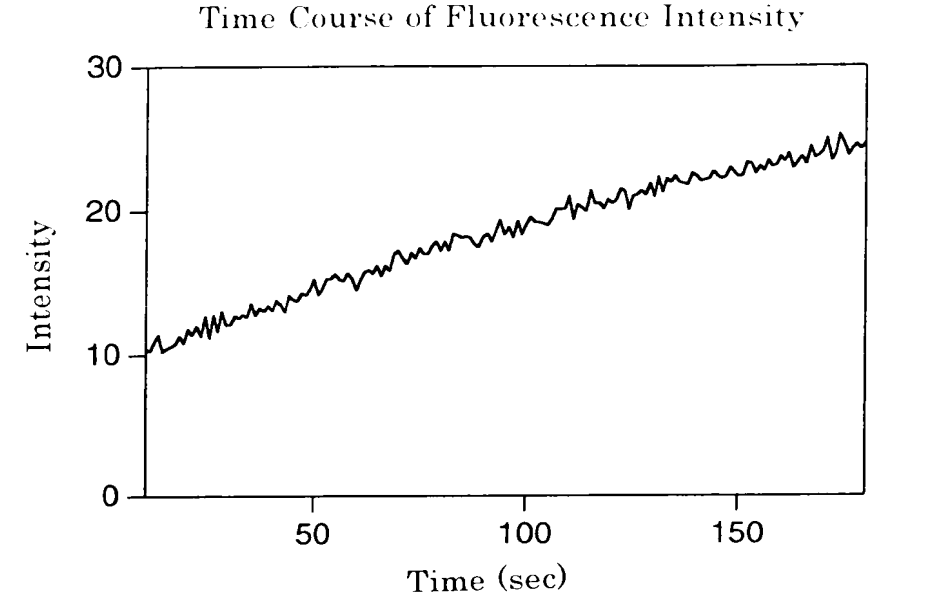

Substrate DNA : Etheno-labeled bovine thymus ssDNA (ε DNA)
Etheno
RecJ
Fluorescence Spectrum
Fluorescence intensity
2000
1500
1000
500
0
200 min
+ RecJ, 20 min
ε DNA
350
400
450
500
Wavelength (nm)

Fig.22


Time Course of Fluorescence Intensity
30
20
10
0
Intensity
50
100
150
Time (sec)

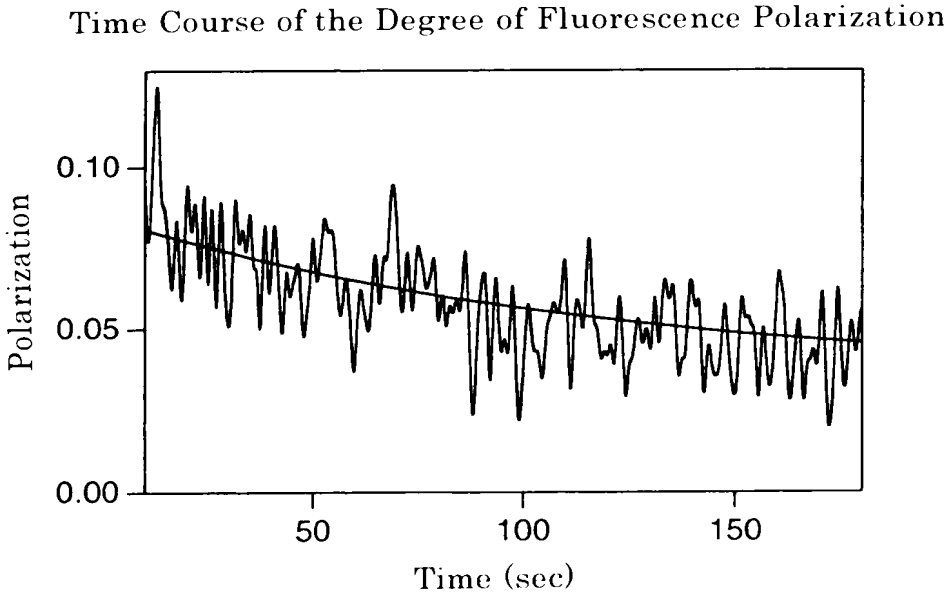

Time Course of the Degree of Fluorescence Polarization
0.10
0.05
0.00
Polarization
50
100
150
Time (sec)

Fig.23

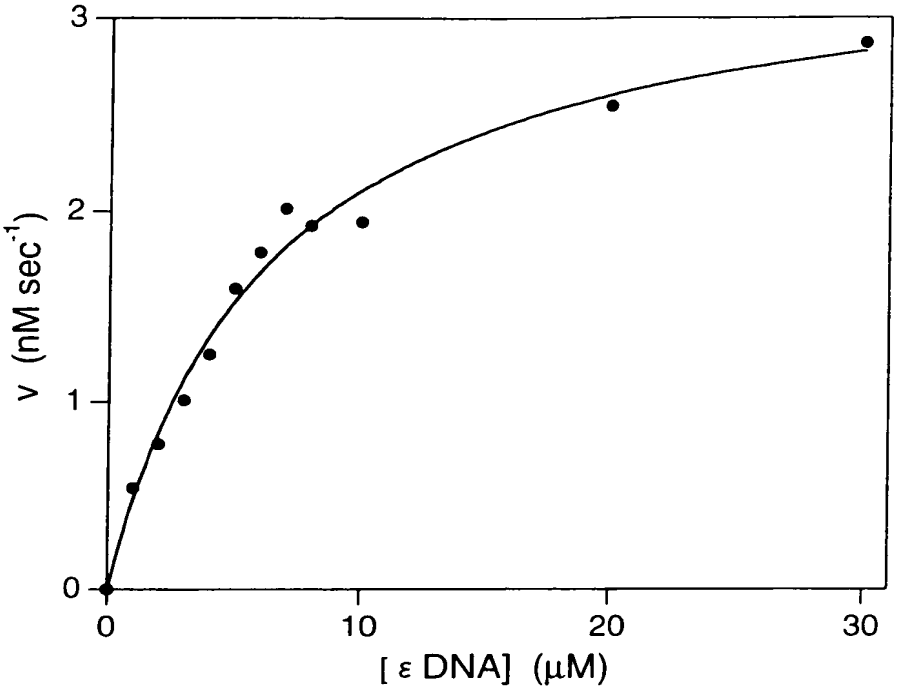


Fig.24

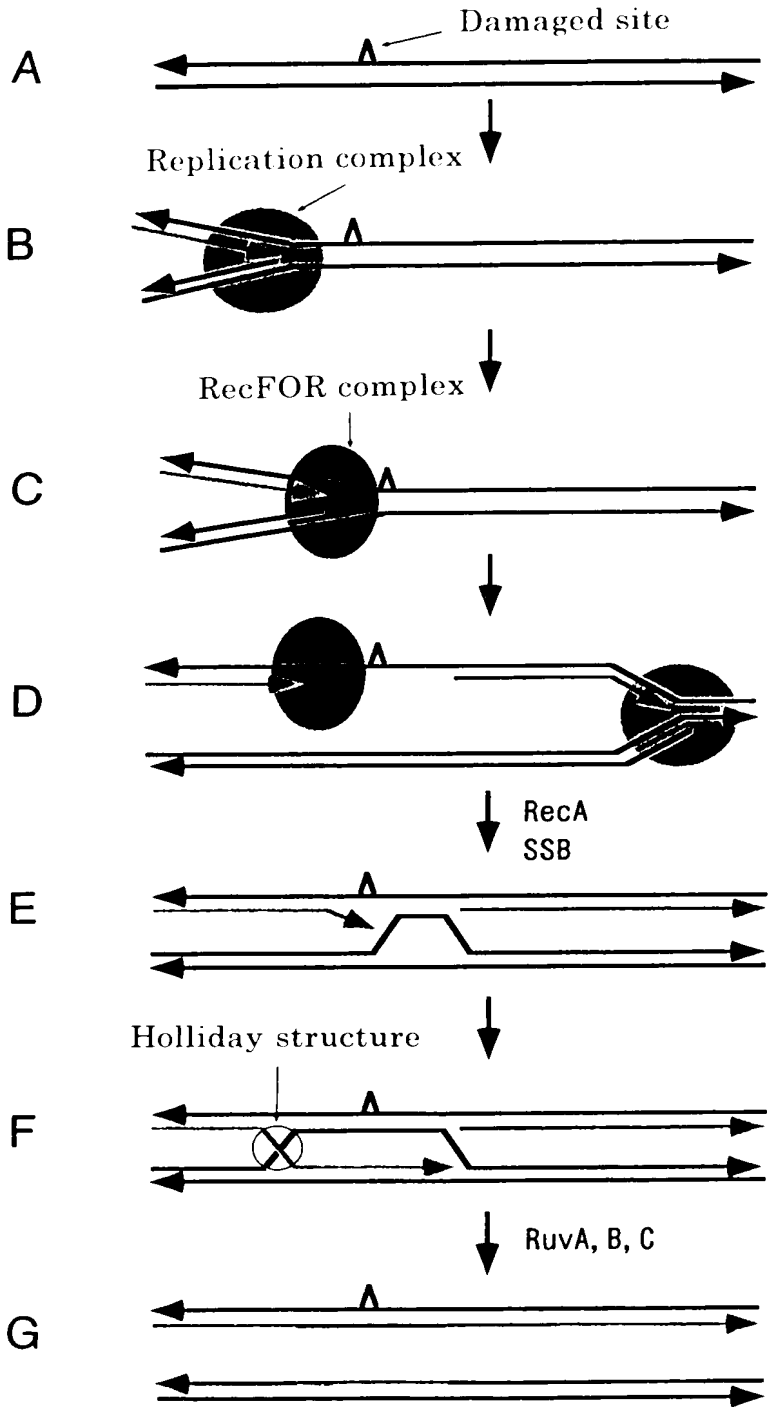

A
Damaged site
Replication complex
B
RecFOR complex
C
D
RecA
SSB
E
Holliday structure
F
RuvA, B, C
G

Fig.25

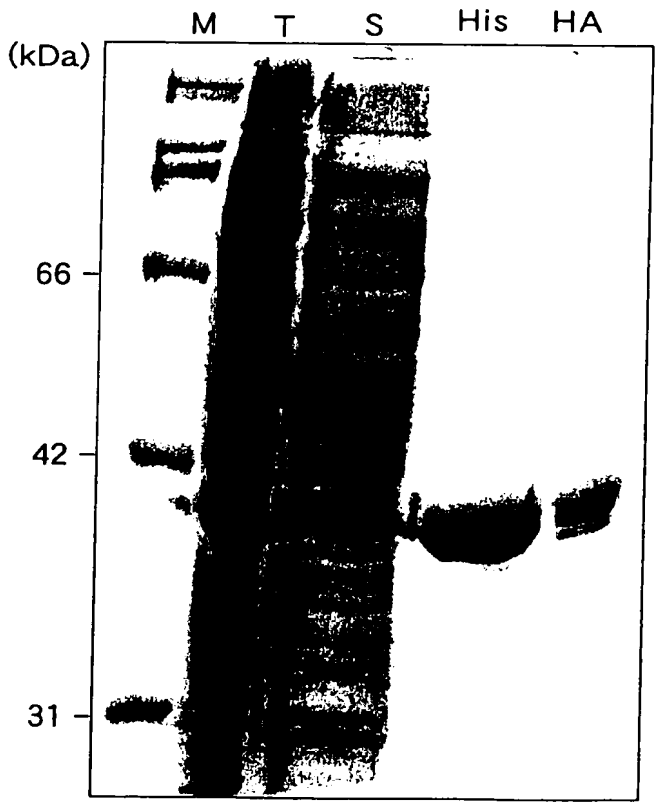


Fig.26

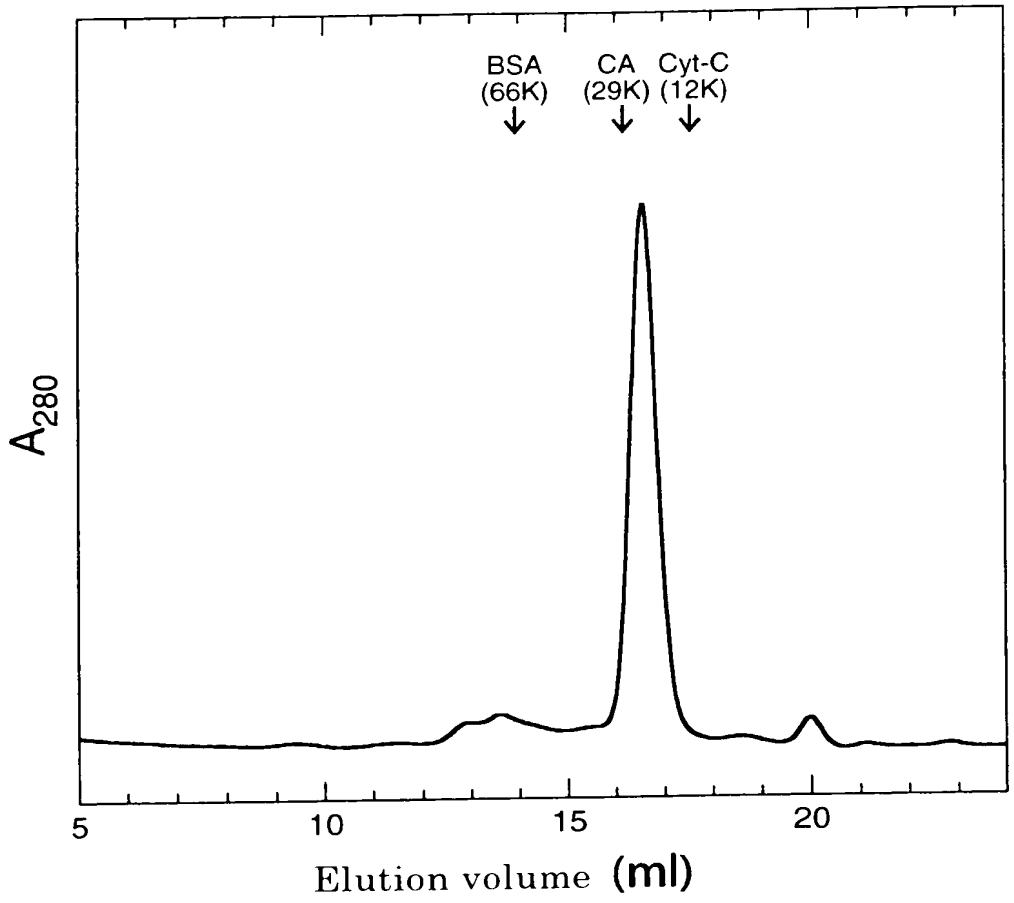
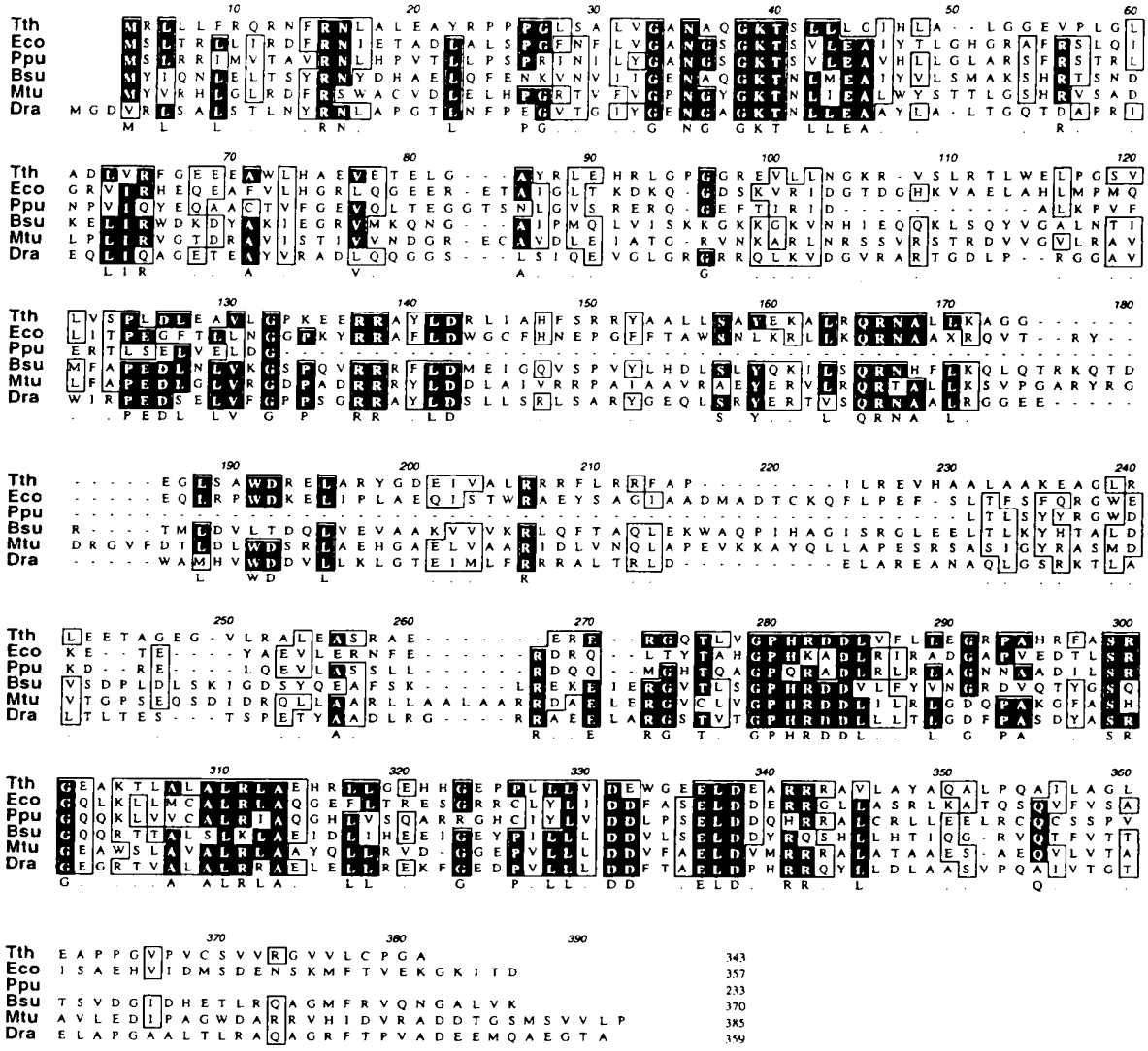


Fig.27



Tth: *Thermus thermophilus* HB8

Eco: *Escherichia coli*

Ppu: *Pseudomonas putida*

Bsu: *Bacillus subtilis*

Mtu: *Mycobacterium tuberculosis*

Dra: *Deinococcus radiodurans*

Fig.28

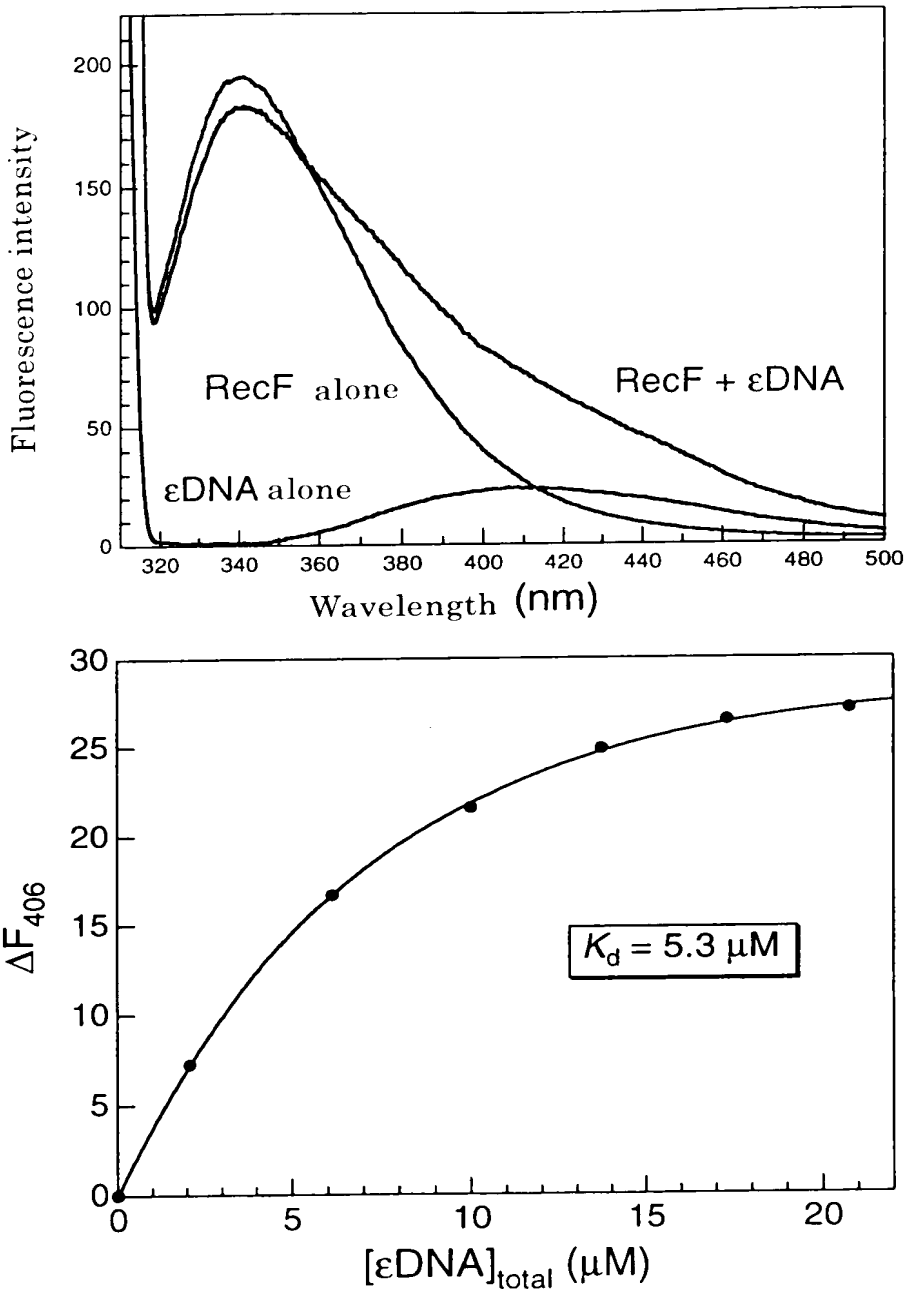

Fluorescence intensity
200
150
100
50
0
320
340
360
380
400
420
440
460
480
500
Wavelength (nm)
RecF alone
RecF + εDNA
εDNA alone
ΔF406
30
25
20
15
10
5
0
0
5
10
15
20
[εDNA]total (μM)
Kd = 5.3 μM

Fig.29

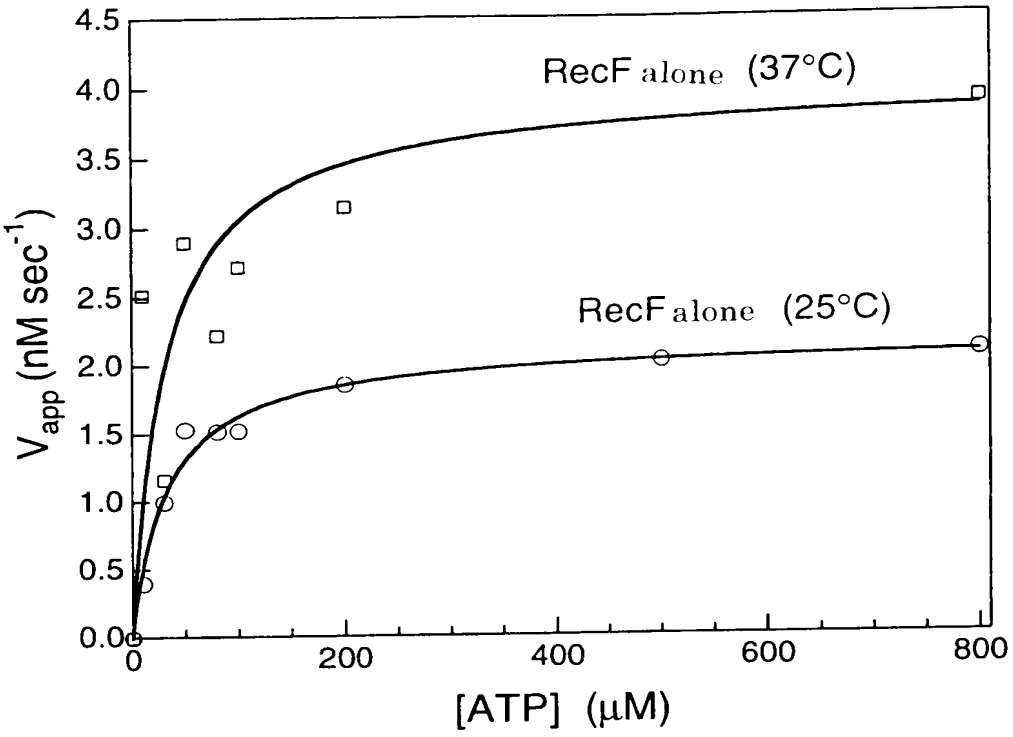

RecF alone (37°C)
RecF alone (25°C)
V_{app} (nM sec^{-1})
[ATP] (μM)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
0
200
400
600
800

Fig.30

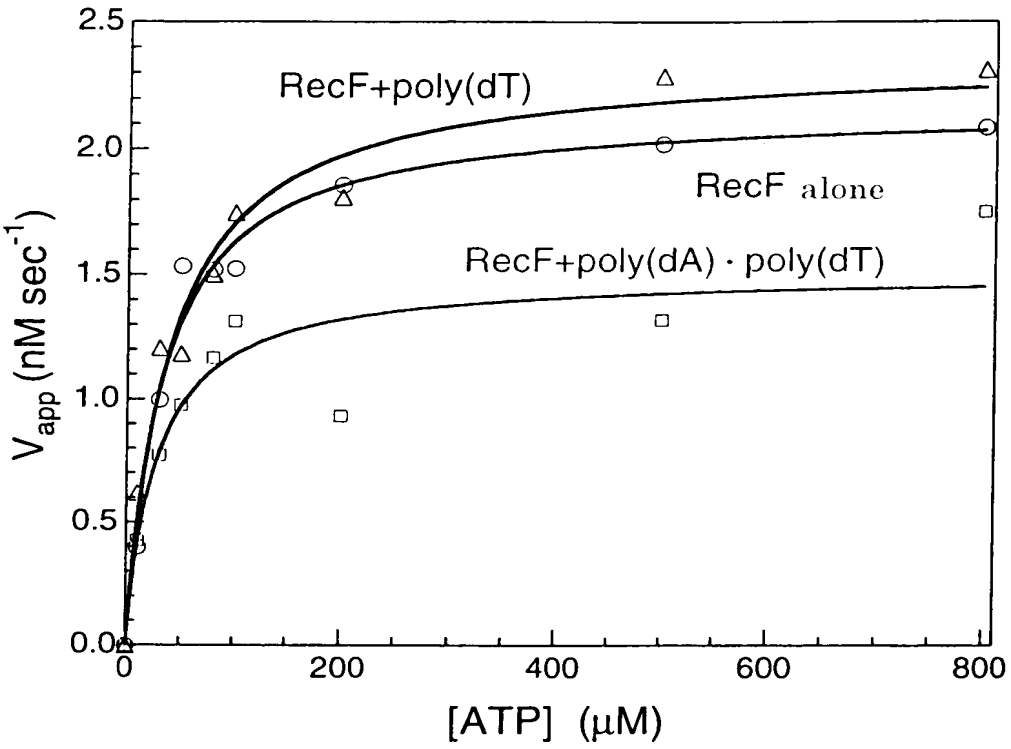

RecF+poly(dT)
RecF alone
RecF+poly(dA) · poly(dT)
V_{app} (nM sec^{-1})
[ATP] (μM)
0.0
0.5
1.0
1.5
2.0
2.5
0
200
400
600
800

Fig.31

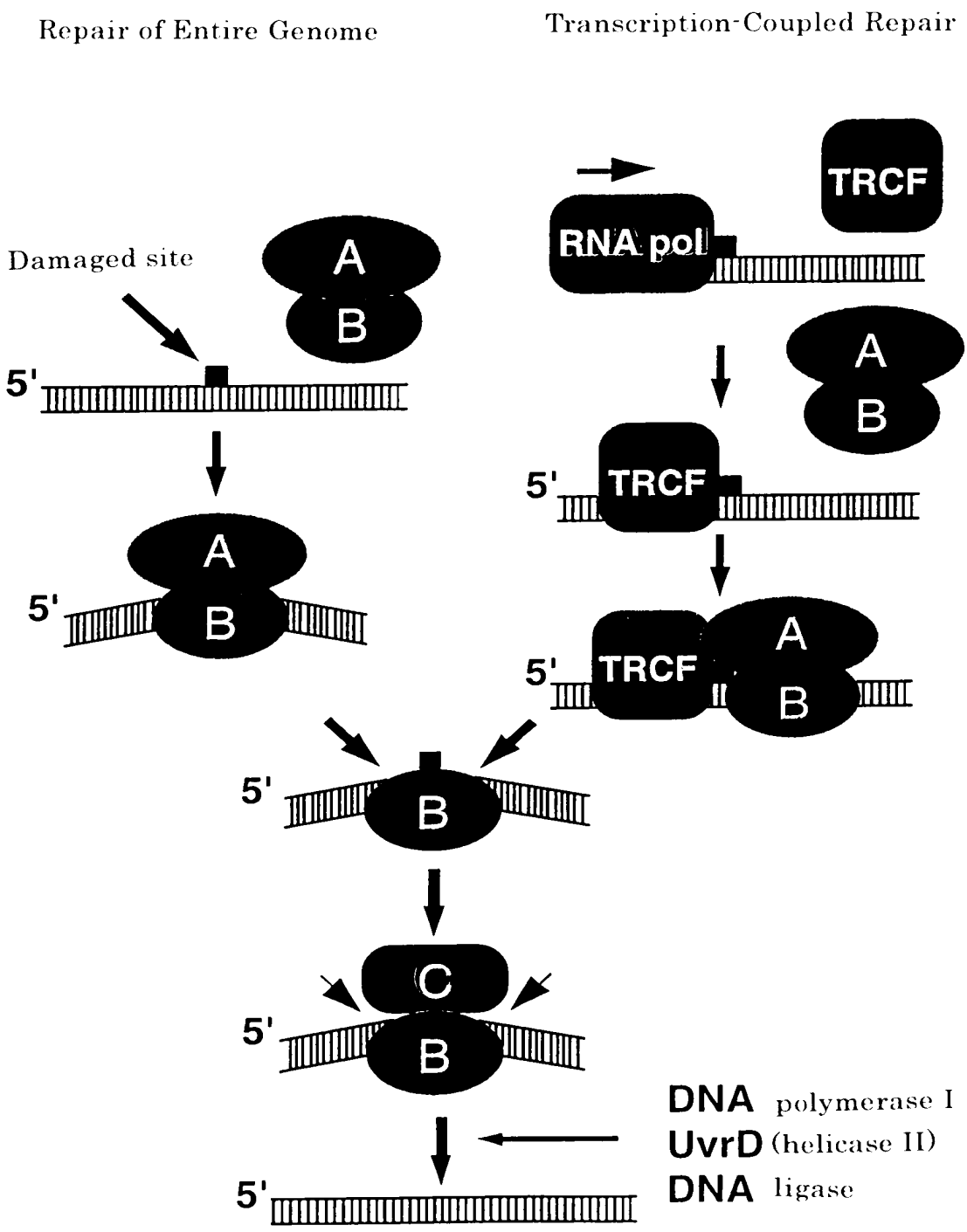

Repair of Entire Genome
Transcription-Coupled Repair
Damaged site
A
B
5'
TRCF
RNA pol
C
DNA polymerase I
UvrD (helicase II)
DNA ligase

Fig.32

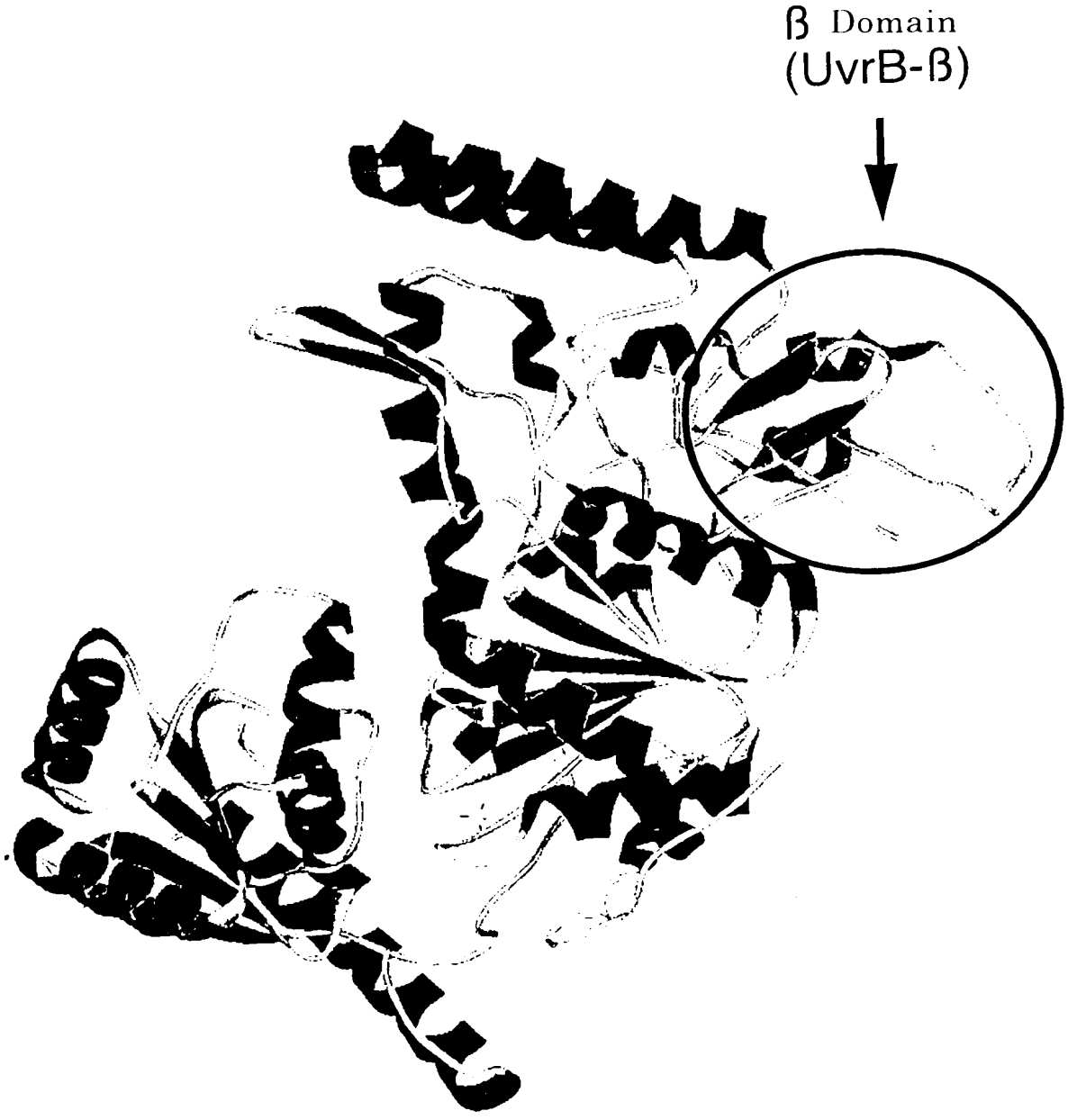
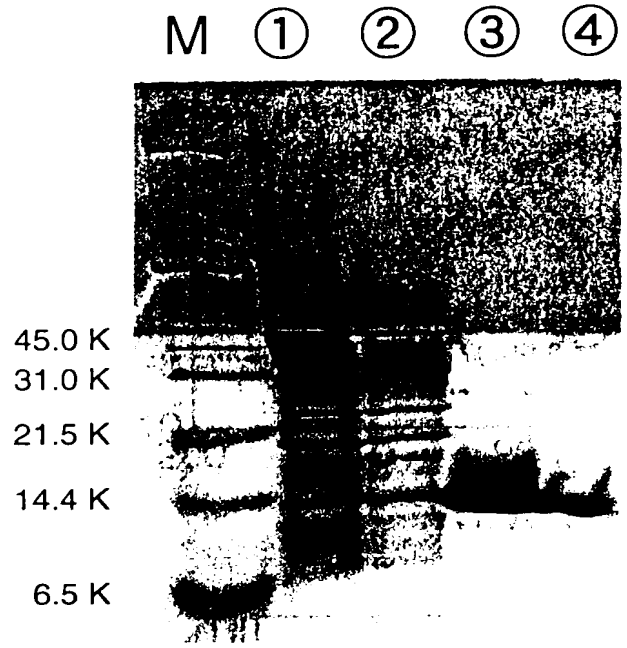


Fig.33

UvrB-ß



TRCF-ß

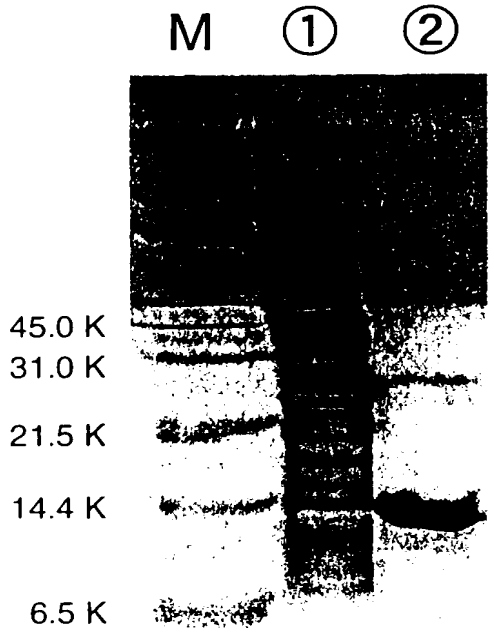
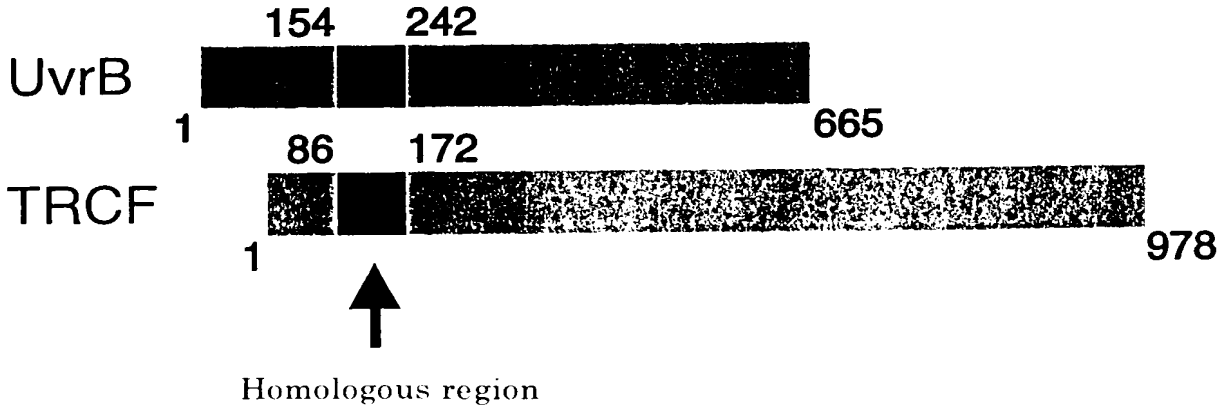


Fig.34

```
UvrB-β  154 RNLVVERGKPYPREVLLERLLELGYQRNDI 184
TRCF-β   86 WRLLLEVGRAYPREALLSRLLKLGYAR--- 113
                *..* *. **** ** *** *** *

UvrB-β  185 DLSPGRFRAKGEVLEIFPAYETEPIRVELF 215
TRCF-β  114 DED---YRVLGEVVELG------EVRLEFF 148
            *     .*  ***.*.         .*.* *

UvrB-β  216 GDEVERISQVHPVTG-ERLRELPG------ 236
TRCF-β  149 GDELERLVVRGEERRRHVLLPKPGKAEGFT 163
            ***.**             *   **

UvrB-β  237 ---FVLFPA 242
TRCF-β  164 SKKVLHFPG 172
              .  **
```

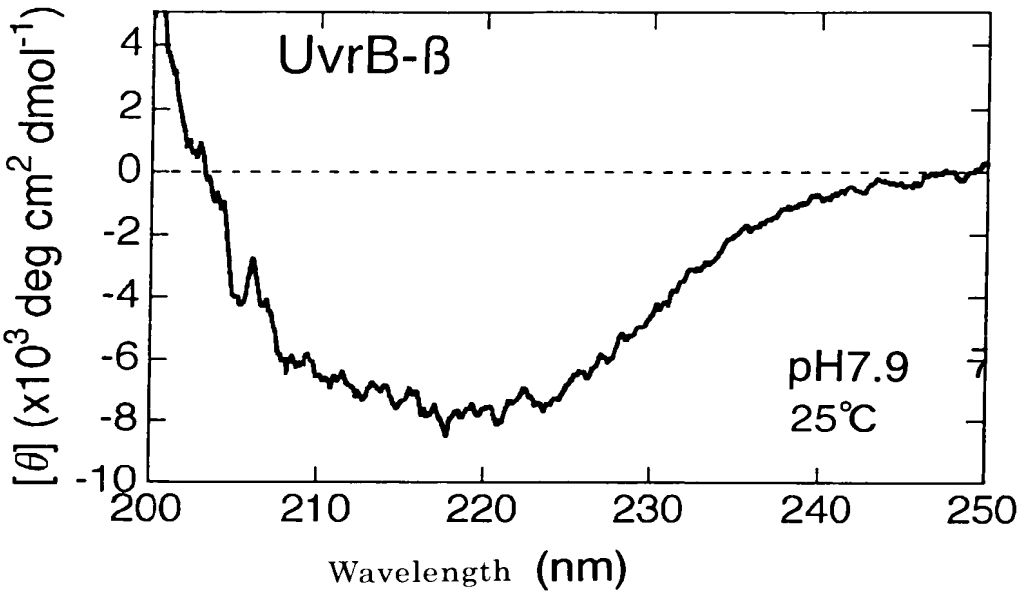
* Identical amino acid residues

. Homologous amino acid residues



Homologous region

Fig.35


UvrB-ß
pH7.9
25℃
[θ] (x10^3 deg cm^2 dmol^-1)
4
2
0
-2
-4
-6
-8
-10
200
210
220
230
240
250
Wavelength (nm)

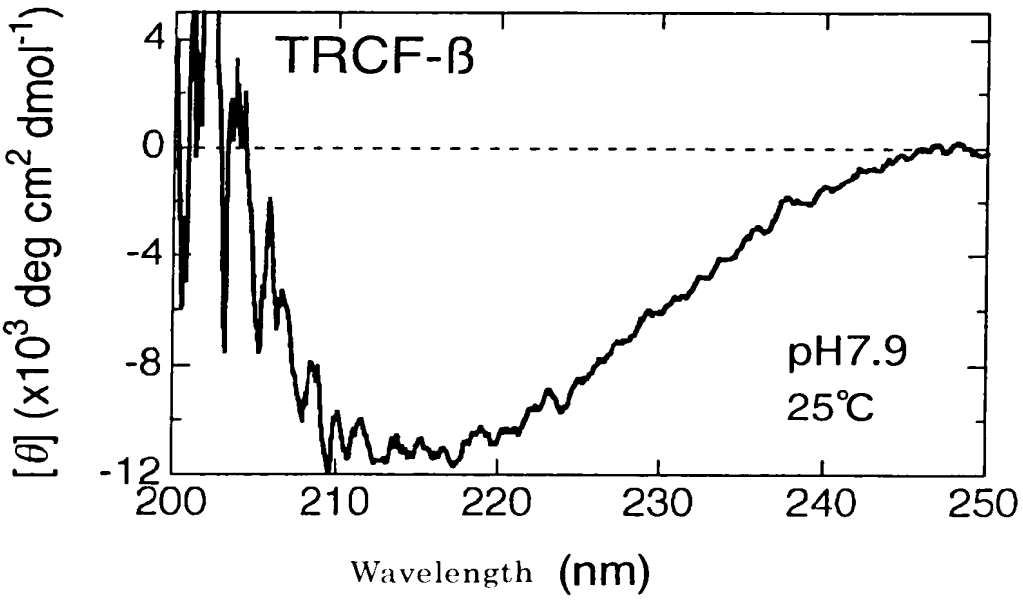

TRCF-ß
pH7.9
25℃
[θ] (x10^3 deg cm^2 dmol^-1)
4
0
-4
-8
-12
200
210
220
230
240
250
Wavelength (nm)

Fig.36

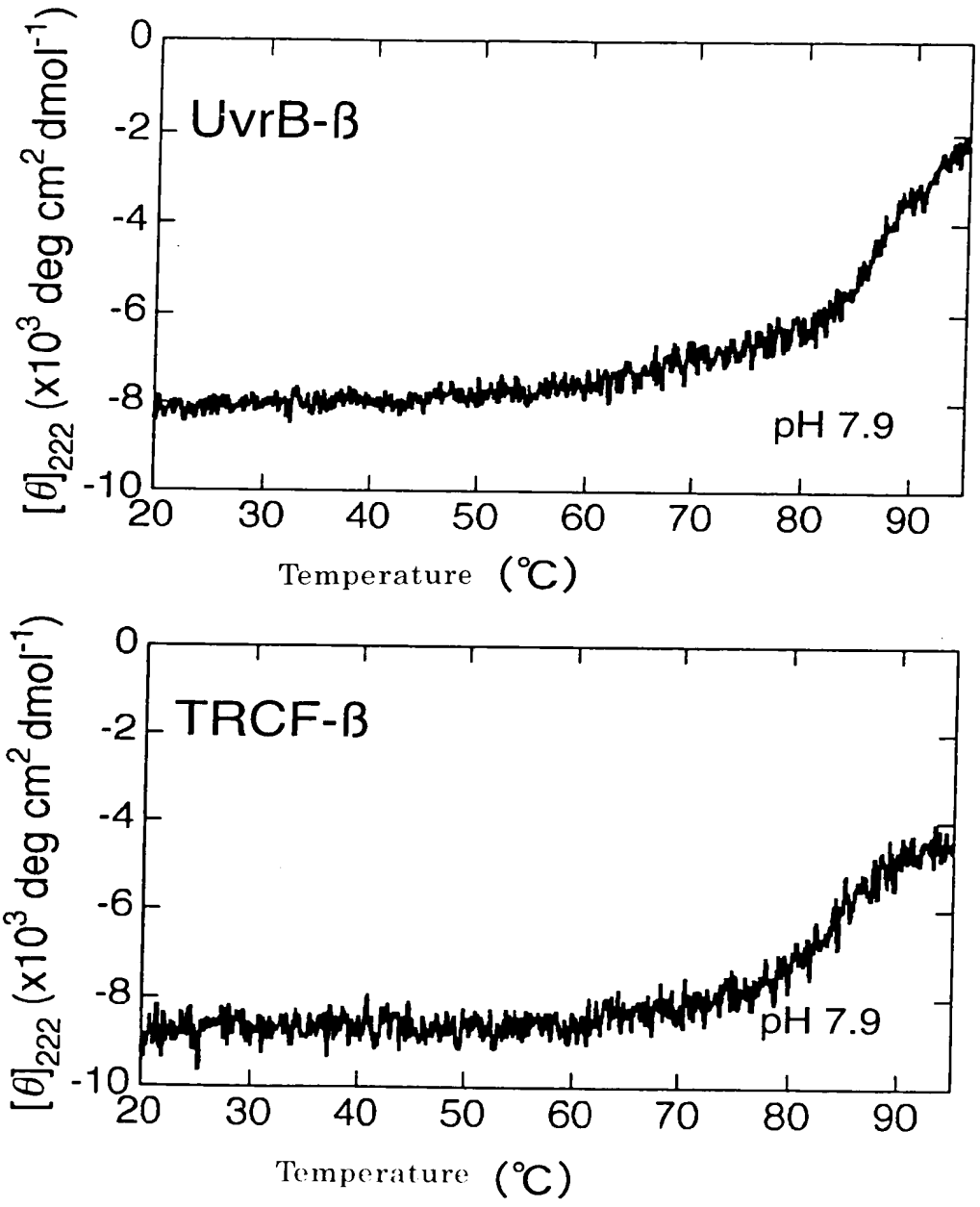

UvrB-β
pH 7.9
$[\theta]_{222}$ (x10^3 deg cm^2 dmol^{-1})
0
-2
-4
-6
-8
-10
20
30
40
50
60
70
80
90
Temperature (℃)
TRCF-β
pH 7.9
$[\theta]_{222}$ (x10^3 deg cm^2 dmol^{-1})
0
-2
-4
-6
-8
-10
20
30
40
50
60
70
80
90
Temperature (℃)

Fig.37

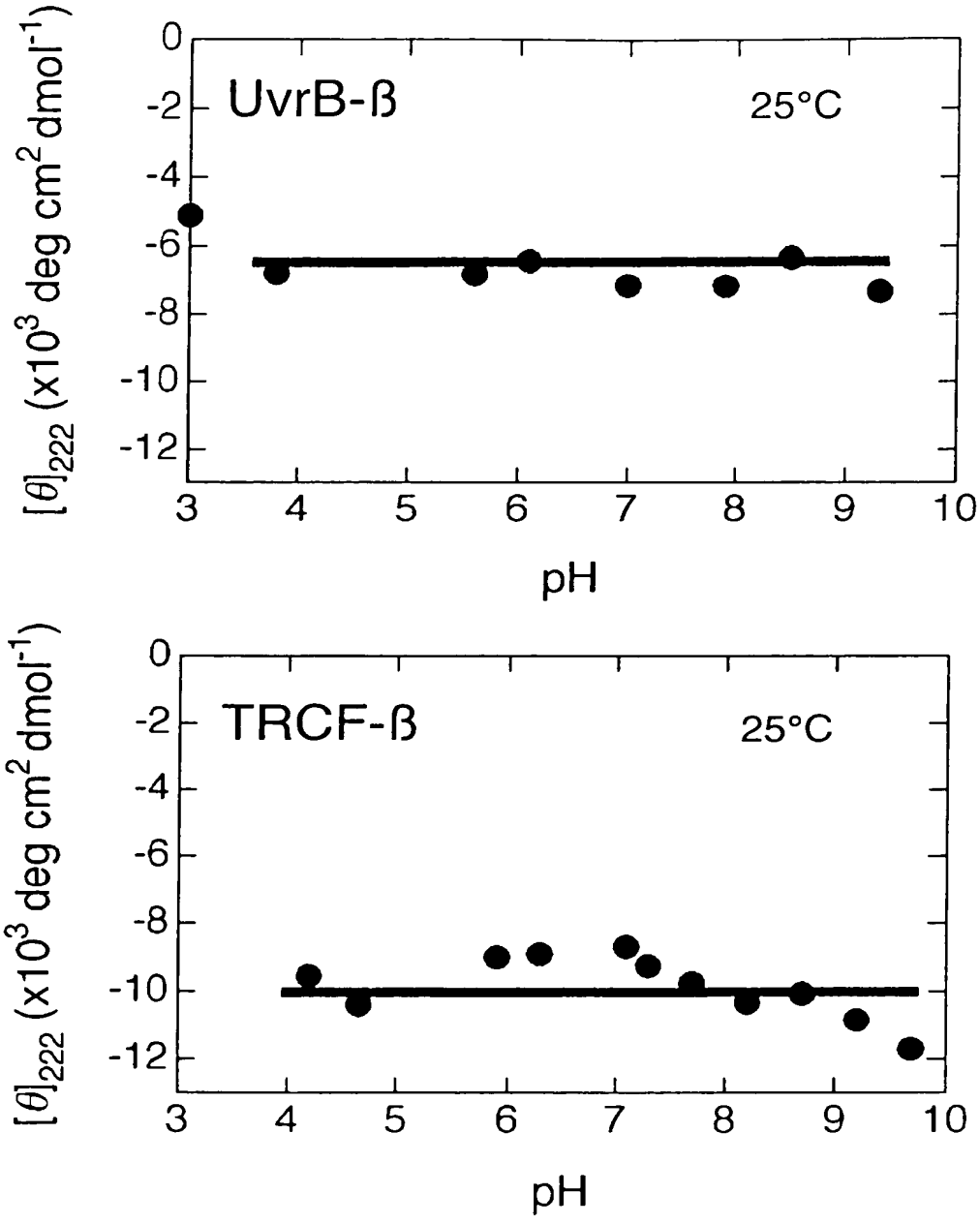

UvrB-ß
25°C
$[\theta]_{222}$ (x10^3 deg cm^2 dmol^{-1})
0
-2
-4
-6
-8
-10
-12
3
4
5
6
7
8
9
10
pH
TRCF-ß
25°C
$[\theta]_{222}$ (x10^3 deg cm^2 dmol^{-1})
0
-2
-4
-6
-8
-10
-12
3
4
5
6
7
8
9
10
pH

Fig.38

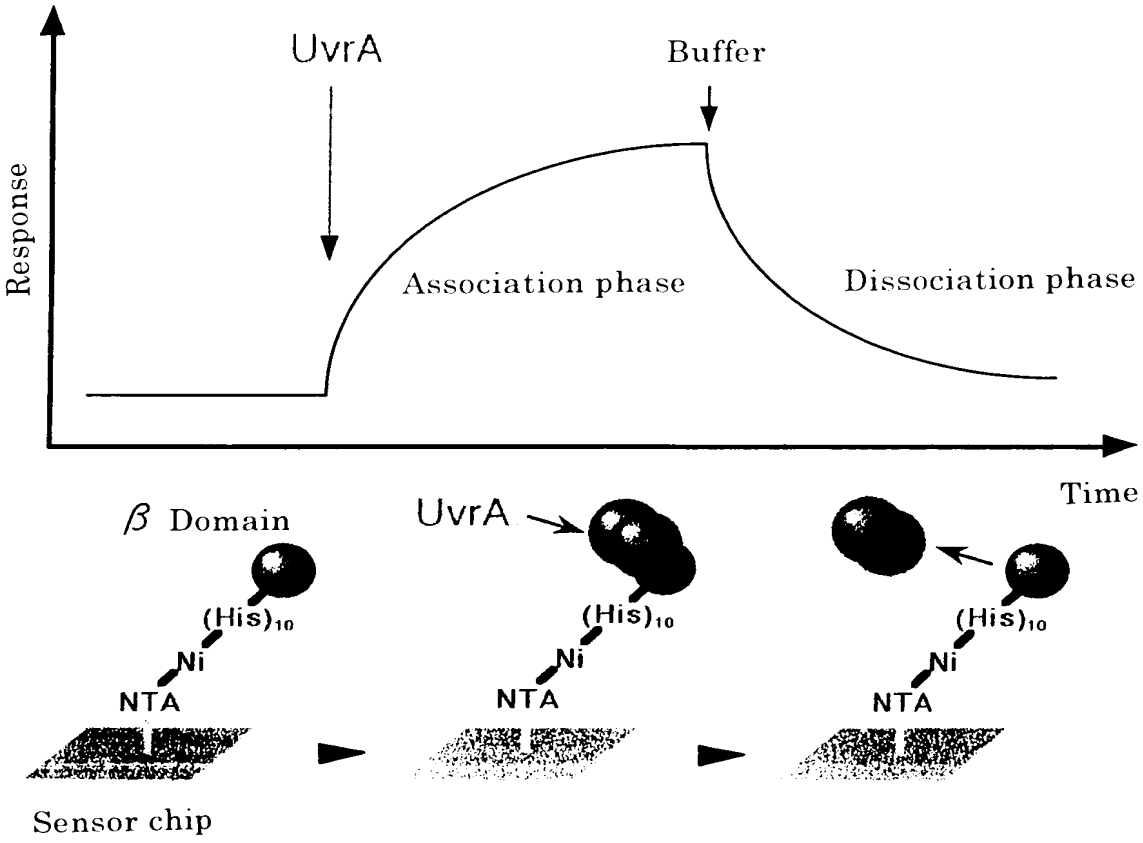
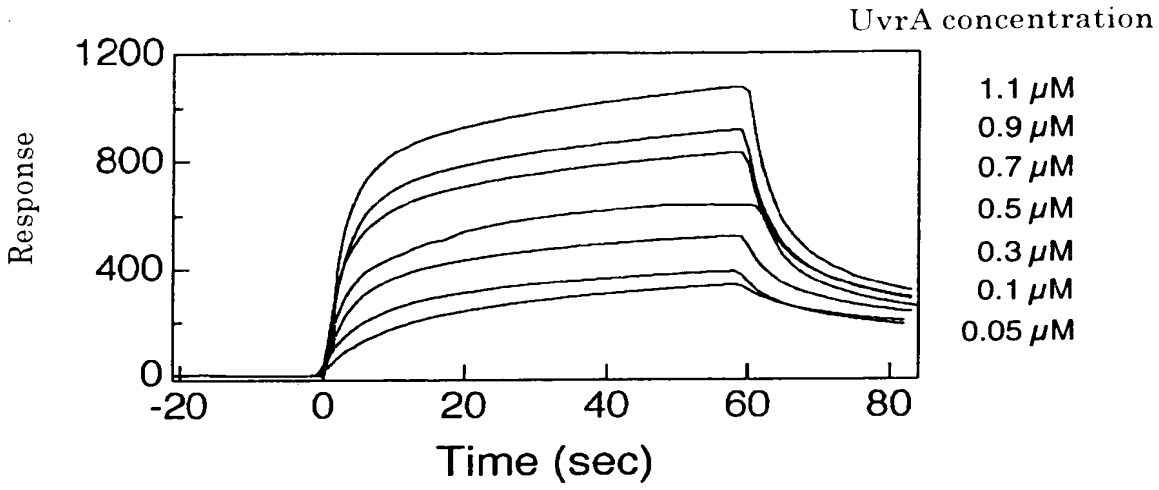

UvrA
Buffer
Response
Association phase
Dissociation phase
Time
β Domain
UvrA
(His)10
Ni
NTA
(His)10
Ni
NTA
(His)10
Ni
NTA
Sensor chip

Fig.39

Sensorgram



Analytical Results

	K_d (x10^{-6} M)		k_{on} (x10^5 M^{-1}S^{-1})		k_{off} (x10^{-1} S^{-1})	
	- ATP	+ ATP	- ATP	+ ATP	- ATP	+ ATP
UvrB-ß	2.6	0.4	2.0	1.5	5.2	0.6
TRCF-ß	1.3	0.5	1.0	1.5	1.3	0.7